

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 27, 2004, 20:55:20 ; Search time 23 Seconds

(without alignments)
445,992 Million cell updates/sec

Title: US-09-626-219-1

Perfect score: 1133

Sequence: 1 SQPQAVPPYASNTCRDQF.....QSDTCKNPLEPPEPMSGT 197

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1133	100.0	435	1	TNR3_HUMAN
2	771	68.0	415	1	TNR3_MOUSE
3	305	26.9	461	1	TR1B_HUMAN
4	295	26.0	474	1	TR1B_MOUSE
5	285.5	25.2	300	1	TR6B_HUMAN
6	283	25.0	625	1	TR1L_MOUSE
7	278	24.5	277	1	TNR5_HUMAN
8	277	24.4	616	1	TR1L_HUMAN
9	251.5	22.2	269	1	TNR5_BOVIN
10	243.5	21.5	289	1	TNR5_MOUSE
11	242.5	21.4	401	1	TR1B_MOUSE
12	239.5	21.1	401	1	TR1B_HUMAN
13	235.5	20.8	401	1	TR1B_MOUSE
14	230.5	20.3	283	1	TR14_HUMAN
15	228.5	20.2	655	1	TR21_HUMAN
16	226.5	20.0	655	1	TR21_MOUSE
17	225	19.9	349	1	CRMB_MOUSE
18	222.5	19.6	271	1	TNR4_MOUSE
19	214.5	18.9	272	1	TNR4_MOUSE
20	210.5	18.6	455	1	TR14_HUMAN
21	210	18.5	349	1	CRMB_MOUSE
22	207	18.3	351	1	CRMB_MOUSE
23	206	18.2	461	1	TR1A_MOUSE
24	203	17.9	323	1	TNR6_BOVIN
25	201	17.7	277	1	TNR4_HUMAN
26	201	17.3	454	1	TR1A_MOUSE
27	196	17.3	595	1	TNR8_HUMAN
28	195.5	17.3	255	1	TNR9_HUMAN
29	194	17.1	332	1	TNR6_MOUSE
30	189	16.7	325	1	TR2_MOUSE
31	188	16.6	471	1	TR1A_BOVIN
32	184.5	16.3	461	1	TR1A_MOUSE
33	183.5	16.2	326	1	TR2_MOUSE

34	182	16.1	498	1	TNR8_MOUSE	Q60846 mus musculus
35	181	16.0	335	1	TNR6_HUMAN	P25445 homo sapien
36	179.5	15.8	256	1	TNR6_MOUSE	P20334 mus musculus
37	171.5	15.1	425	1	TR1B_MOUSE	P07174 rattus norv
38	167.5	14.8	440	1	TR1B_HUMAN	O14763 homo sapien
39	166	14.7	493	1	TNR6_MOUSE	P97525 rattus norv
40	164	14.5	416	1	TR16_CHICK	P18519 gallus gall
41	162	14.3	327	1	TNR6_MOUSE	P25446 mus musculus
42	152.5	13.5	417	1	TR16_MOUSE	Q920W1 mus musculus
43	148.5	13.1	427	1	TR16_HUMAN	P08138 homo sapien
44	145.5	12.8	324	1	TR1B_MOUSE	Q63199 rattus norv
45	145	12.8	198	1	TR2_MOUSE	Q920W2 mus musculus

ALIGNMENTS

RESULT 1

ID	TNR3_HUMAN	STANDARD	PRT	435 AA.
AC	P36941			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 3 precursor			
DE	(lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related protein)			
GN	LYBR OR TNFRSF3 OR TNFR.			
OS	Homo sapiens (human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI TaxID=9606;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=93252381; PubMed=8486360;			
RA	Haens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.,			
RT	"Construction and evaluation of a hncDNA library of human 12p			
RT	transcribed sequences derived from a somatic cell hybrid."			
RL	Genomics 16:214-218 (1993).			
RC	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RX	MEDLINE=2238257; PubMed=12477932;			
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Schmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,			
RA	Villalón D., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Fahy J., D'Elton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M.,			
RA	Butterfield Y.S., Schin J.E., Jones S.J.M., Skalska U., Skallus D.E.,			
RA	Schneher A., Schin J.E., Jones S.J.M., Skalska U., Skallus D.E.,			
RT	"Generation and initial analysis of more than 15,000 full-length			
RT	human and mouse cDNA sequences."			
RP	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RP	[3]			
RP	FUNCTION.			
RX	MEDLINE=94225209; PubMed=8171323;			
RA	Crowe P.D., Vandersdale T.L., Walter B.N., Ware C.F., Hession C.,			
RA	Ehrenfelds B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.,			
RT	"A lymphotoxin-beta-specific receptor."			
RL	Science 264:707-710 (1994).			
RP	[4]			
RP	CHARACTERIZATION.			

RA		MEHLIN-99223511; PubMed=10207006;
RX	Mu M.-Y., Wang P.-X., Han S.-H., Hsieh S.-L.;	
RT	"The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell	
RL	death in HeLa cells."	
RM	J. Biol. Chem. 274:11868-11873 (1999).	
RN	[5]	
RP	FUNCTION.	
RX	MEDLINE=20261554; PubMed=10799510;	
RA	Rooney I.A., Butrovich K.D., Glaes A.A., Borboroglu S., Benedict C.A.,	
RA	Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;	
RT	"The lymphotoxin-beta receptor is necessary and sufficient for	
RL	light-mediated apoptosis of tumor cells."	
RM	J. Biol. Chem. 275:14307-14315 (2000).	
RN	[6]	
RP	INTERACTION WITH TRAF3.	
RX	MEDLINE=96278943; PubMed=8663299;	
RA	Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,	
RA	Yagita H., Okumura K.;	
RT	"TRAF5, an activator of NF-kappaB and putative signal transducer for	
RL	the lymphotoxin-beta receptor."	
RM	J. Biol. Chem. 271:14661-14664 (1996).	
RN	[7]	
RP	INTERACTION WITH TRAF4.	
RX	MEDLINE=98289299; PubMed=9626059;	
RA	Krajevsky M., Krajevski S., Zapata J.M., Vanarsdale T.,	
RA	Gascoyne R.D., Berern K., McFadden D., Shabaik A., Hugh J.,	
RA	Reynolds A., Clevers C.V., Reed J.C.;	
RT	"TRAF-4 expression in epithelial progenitor cells. Analysis in normal	
RL	adult, fetal, and tumor tissues."	
RM	Am. J. Pathol. 152:1549-1561 (1998).	
RN	[8]	
RP	INTERACTION WITH TRAF5.	
RX	MEDLINE=98172745; PubMed=9511754;	
RA	Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,	
RA	Otsuka M., Yamamoto T., Inoue Y.-I.;	
RT	"Cloning and characterization of a cDNA encoding the human homolog of	
RL	tumor necrosis factor receptor-associated factor 5 (TRAF5)."	
Gene	207:135-140 (1998).	
-1-	FUNCTION: Receptor for the heterotrimeric lymphotoxin containing	
CC	LTA and LTb, and for TNFS1A/LIGHT. Promotes apoptosis via TRAF3	
CC	and TRAF5. May play a role in the development of lymphoid organs.	
CC	SUBUNIT: self-associates. Associates with TRAF3, TRAF4 and TRAF5.	
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.	
CC	-1- SIMILARITY: Contains 4 TNFR-Cys repeats.	
CC	-----	
CC	This swiss-prot entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -	
CC	the European Bioinformatics institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See http://www.isb-slb.ch/announce/	
CC	or send an email to license@isb-slb.ch).	
CC	-----	
CC	EMBL; L04270; AAA36757.1; "	
DR	EMBL; BC026262; AAH26262.1; "	
DR	PIR; I54182; I54182.	
DR	HSSP; P25942; 1CDF.	
DR	Genew; HGNC:6718; LTBR.	
DR	MMW; 600979; "	
DR	GO; GO:0007165; P:signal transduction; TAS.	
DR	InterPro; IPR008063; Fas_receptor.	
DR	InterPro; IPR001368; TNFR_c6.	
DR	Pfam; PF000020; TNFR_c6; 4.	
DR	PRINTS; PR01680; FASRECEPTOR.	
DR	SMART; SM00208; TNFR_4.	
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.	
DR	PROSITE; PSS0050; TNFR_NGFR_2; 3.	
KW	Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.	
FT	CHAIN	1 435
FT	SIGNAL	1 30
FT	POTENTIAL.	
FT	TUMOR NECROSIS FACTOR RECEPTOR	
FT	SUPERFAMILY MEMBER 3.	
FT	EXTRACELLULAR (POTENTIAL).	
FT	DOMAIN	31 227
FT	TRANSMEM	228 248
FT		

FT	DOMAIN	249	435	CYTOPLASMIC (POTENTIAL).
FT	REPEAT	42	81	TNR-CYS 1.
FT	REPEAT	82	124	TNR-CYS 2.
FT	REPEAT	125	168	TNR-CYS 3.
FT	REPEAT	169	211	TNR-CYS 4.
FT	DISULFID	43	58	BY SIMILARITY.
FT	DISULFID	59	72	BY SIMILARITY.
FT	DISULFID	62	80	BY SIMILARITY.
FT	DISULFID	83	98	BY SIMILARITY.
FT	DISULFID	101	116	BY SIMILARITY.
FT	DISULFID	104	124	BY SIMILARITY.
FT	DISULFID	126	132	BY SIMILARITY.
FT	DISULFID	139	148	BY SIMILARITY.
FT	DISULFID	142	167	BY SIMILARITY.
FT	DISULFID	170	185	BY SIMILARITY.
FT	CARBOHYD	40	40	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	177	177	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	435 AA;	46709 MW;	624626E6022P656P CXC64;
Query Match			100.0%;	Score 1133; DB 1; Length 435;
Best Local Similarity			100.0%;	Pred. No. 9,1e-90;
Matches 197;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0
QY	1	SQPAVAPVASENQTCDPEKEVEYEPORHICCSRCPPGTYSYSAKCSRIIDTVYCATCAENS	60	
Db	28	SQPAVAPVASENQTCDPEKEVEYEPORHICCSRCPPGTYSYSAKCSRIIDTVYCATCAENS	87	
QY	61	YNEHNVYITTCQLCPDPPVWGLEIAPCTSKRTQCCQCPGFCAMALBCTHCELLSD	120	
Db	88	YNEHNVYITTCQLCPDPPVWGLEIAPCTSKRTQCCQCPGFCAMALBCTHCELLSD	147	
QY	121	CPPGTEALKEVGVGNHNCVPCCKRGKHQNTSSPASCOPHTRCENOGIYEAAPGTASD	180	
Db	148	CPPGTEALKEVGVGNHNCVPCCKRGKHQNTSSPASCOPHTRCENOGIYEAAPGTASD	207	
QY	181	TTCKNPLEPLPEPMESGT 197		
Db	208	TTCKNPLEPLPEPMESGT 224		
Db				
RESULT 2				
TNR3_MOUSE				
ID	TNR3_MOUSE	STANDARD;	PRT;	415 AA.
AC	P50784;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 3 precursor			
DE	(Lymphotoxin-beta receptor).			
GN	LTBR OR TNFRSF3 OR TNFCR.			
OC	Mus musculus (Mouse); Chordata; Vertebrata; Euteleostomi;			
OC	Eukaryota; Metazoa; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CWR; TISSUE=Lung;			
RX	MEDLINE=96072804; Pubmed=7594541;			
RA	Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,			
RA	Browning J.L., Ware C.F.;			
RT	"Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,			
RT	and expression.";			
RL	J. Immunol. 155:5280-5288(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96163885; Pubmed=8586432;			
RA	Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,			
RA	Honjo T.;			
RT	"The murine lymphotoxin-beta receptor cDNA: isolation by the signal			
RT	sequence trap and chromosomal mapping.";			
RL	Genomics 30:312-319(1995).			
RN	[3]			
RP	INTERACTION WITH TRAF5.			

RC STRAIN=BALB/c;
 RX MEDLINE=96278943; PubMed=8663299;
 RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
 RA Yagita H., Okumura K.;
 RT "TRAF5, an activator of NF-kappaB and putative signal transducer for
 RT the lymphotoxin-beta receptor.";
 RL J. Biol. Chem. 271:14661-14664(1996).
 CC -1- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
 CC LTA and LTb, and for TNFb14/LIGHT. Promotes apoptosis via TRAF5
 CC and TRAF5. May play a role in the development of lymphoid organs
 CC (By similarity).
 CC -1- SUBUNIT: Self-associates (By similarity). Associates with TRAF5.
 CC Associates with TRAF3 and TRAF4 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>
 CC or send an email to license@ebi.ac.uk).

CC -----
 DR EMBL; U29173; AAA68964.1; -;
 DR EMBL; L38423; AAB00846.1; -;
 DR EMBL; U30798; AAA81334.1; -;
 DR HSSP; 014763; 1D0G.
 DR MGD; MGI:104875; Ltbt.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR SMART; SMO0208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS00500; TNFR_NGFR_2; 3.
 KM Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 PT SIGNAL 1 30
 FT CHAIN 31 415
 FT FT
 FT FT
 FT DOMAIN 31 223
 FT TRANSMEM 224 244
 FT DOMAIN 245 415
 FT REPEAT 42 81
 FT REPEAT 82 124
 FT REPEAT 125 170
 FT REPEAT 171 213
 FT DISULFID 43 58
 FT DISULFID 59 72
 FT DISULFID 73 80
 FT DISULFID 83 98
 FT DISULFID 101 116
 FT DISULFID 104 124
 FT DISULFID 126 132
 FT DISULFID 139 150
 FT DISULFID 142 169
 FT DISULFID 172 187
 FT CARBOHYD 40 40
 FT CARBOHYD 179 179
 SQ SEQUENCE 415 AA, 44956 MW, 298326A56A6E661 CRC64;
 Query Match 68.0%; Score 771; DB 1; Length 415;
 Best Local Similarity 70.7%; Pred. No. 7.1e-59;
 Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;

QY 1 SOPAVVPYASNGTCRODEKRYEPQHRICCSRCPPGTYSAKSRIRDTVCATCAANS 60
 Db 28 SOPQIVPPIRIENQTCWQDQKXYEPHMDVCCSRCPGPFVAVCSRGQDITVCKTCHNS 87
 QY 61 YNEHNRYLTICOLGCPDPMGLERLACTSKTKQCQCPQPMFCAWALACTHC-ELI 118
 Db 88 YNEHNHLSITCOLGCPDPIVLSFEVAPPTSRKACRCQCPQMSCVYLDNECVCHCEERL 147
 QY 119 SDCPGTEALEKDEVGKNNHCVPCKAGHFONTSSPSPARCOPHTCENQGLVEAAGTQAQ 178

Db 148 VLCPGTEAETDEIMDVNVCPCPKGHPONTSSPARCOPHTRCETQGLVEAAGTQSY 207
 QY 179 SDTCCKNPLEP 189
 Db 208 SDTCCKNPLEP 218

RESULT 3
 ID TRIB HUMAN STANDARD; PRT; 461 AA.
 AC P20333; Q16042; Q901H1.
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
 DE necrosis factor receptor 2) (p80) (TNF-R2) (p75) (CD120b) (Etanercept)
 GN [contains: tumor necrosis factor binding protein 2 (TBP2)].
 OS TNFRSF1B OR TNFR2 OR TNFR.
 OC Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90260639; PubMed=2160731;
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
 RA Dower S.K., Cosman D., Goodwin R.G.;
 RT "A receptor for tumor necrosis factor defines an unusual family of
 RT cellular and viral proteins.";
 RL Science 248:1019-1023(1990).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANT ARG-196.
 RX MEDLINE=91045991; PubMed=2172983;
 RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
 RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
 RT "A second tumor necrosis factor receptor gene product can shed a
 RT naturally occurring tumor necrosis factor inhibitor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9629745; PubMed=8661109;
 RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
 RA Lepelletier D., Stallard B.J., Goeddel D.V., Desautels F.J.;
 RA Brodeur G.M.;
 RT "Physical mapping and genomic structure of the human TNFR2 gene.";
 RL Genomics 35:94-100(1996).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANTS ARG-196; LYS-232; PRO-269 AND
 RP ARG-301.
 RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Wiltrak L.A., Nickerson D.A.;
 RL Submitted (Mar-2003) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PNS;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Utsin T.B., Toshiki S., Carninci P., Prange C.,
 RA Bosak S.A., McEwan L.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,


```

Db 86 LMNWPBCLSCGSSRSSQV-----ETQACTBQRNICTCRGOWTCALSKQBGCRICADLR 141
QY 120 DCPPE-----TEALIKDEVGKNNHCVPCKAGHPONTSSPARCOPHTRCENOGIVEAP 174
Db 142 KCRGFGVARDGTETSDV-----CKRCAGTGFSTNTSSDIDCRPHQICN-----VVAIP 191
QY 175 GTAQSDTTC-KNPLEPRLP 192
Db 192 GNASMDAVCTSTSTPSRMAP 211

RESULT 4
TRIM MOUSE
ID TRIB_MOUSE STANDARD; PRT; 474 AA.
AC P25119; P97893;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
  necrosis factor receptor 2) (TNFR-2) (p75).
GN TNFRSF1B OR TNFR2 OR TNFR-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=918785; PubMed=1849278;
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
  Wong G.H., Chen E.Y., Goeddel D.V.;
RT "Cloning and expression of cDNAs for two distinct murine tumor
  necrosis factor receptors demonstrate one receptor is species
  specific."
RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91246168; PubMed=1645445.
RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
  Copeland N.G., Jenkins N.A., Smith C.A.;
RT "Molecular cloning and expression of the type 1 and type 2 murine
  receptors for tumor necrosis factor."
RL Mol. Cell. Biol. 11:3020-3026(1991).
RN [3]
RP SEQUENCE OF 1-26 FROM N.A.
RC STRAIN=NOD;
RA Jacob C.O., Liu J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-22 FROM N.A.
RC TISSUE=Liver;
RA Kissingerhis M., Fellows R., Feldmann M., Chernajovsky Y.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and
  approximately 5-fold lower affinity for homotrimeric
  TNFSF1/lymphotxin-alpha. The TRAF1/TRAF2 complex recruits the
  apoptotic suppressors BIRC2 and BIRC3 to TNFSF1B/TNFR2 (by
  similarity).
CC -1- SUBUNIT: Binds to TRAF2 (by similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M60469; AAA39752.1; -
DR EMBL; M59378; AAA40463.1; -
DR EMBL; U39488; AAA85021.1; -

```

```

DR EMBL; X87128; CAAG6018.1; -
DR PIR; B38634; B38634.
DR HSSP; P19438; INCF.
DR MED; MG1:1314883; Tnfrsf1b.
DR GO; GO:0007716; P:cell surface receptor linked signal transdu. . .; IMP.
DR GO; GO:0006954; P:inflammatory response; IMP.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
KM Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 22
FT CHAIN 23 474
FT FT 23 474
FT DOMAIN 23 258
FT TRANSMEM 259 288
FT DOMAIN 289 474
FT REPEAT 39 77
FT REPEAT 78 119
FT REPEAT 120 164
FT REPEAT 165 203
FT DISULFID 40 54
FT DISULFID 55 68
FT DISULFID 58 76
FT DISULFID 79 94
FT DISULFID 97 111
FT DISULFID 101 119
FT DISULFID 121 127
FT DISULFID 136 145
FT DISULFID 139 163
FT DISULFID 166 181
FT CARBOHYD 69 69
FT CARBOHYD 195 195
SQ SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

Query Match 26.0%; Score 295; DB 1; Length 474;
Best Local Similarity 34.0%; Pred. No. 3,6e-18;
Matches 66; Conservative 24; Mismatches 84; Indels 20; Gaps 8;

QY 8 PYASE-NQTRDDEKEYEPQHRICSRCPGYYSAKSGRIIDYVCATCAENSYEHWN 66
Db 31 PYRPEPGVEEQISQ-HYDRKAMQCCAKCPGQYVHKFKTSDTVACDEASWYQVWN 89
QY 67 YLTICQLCR---PCDPYMGLEELAPCTSKKRTQCRQPGMECA-AALAECHCELISDC 121
Db 90 QPRTCLSSGSSCTTDV---ETRACTKQONRVCAEGAGRYCALKTHSGSCRCQMRLSKC 145
QY 122 PGTEAEIKDEVGKNNHCVPCKAGHPONTSSPARCOPHTRCENOGIVEAPGTASPT 181
Db 146 GPGF-GVASSRAENVGLCKACAGPGRFSDTSTDCRPHRIS-----IIATGNASTDA 200
QY 182 TCNPLEPRLPEPMS 195
Db 201 VC---APESPILS 210

RESULT 5
TRIM HUMAN
ID TRIB_HUMAN STANDARD; PRT; 300 AA.
AC C95407;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6B precursor (Decoy
  receptor for Fas ligand) (Decoy receptor 3) (DCR3) (M68).
GN TNFRSF6B OR DCR3 OR TR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]

```

RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal lung;
 RA MEDLINE=99087326; PubMed=9872321;
 RA Pilti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
 RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
 RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
 RA Goddard A.D., Botstein D., Ashkenazi A.;
 RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
 RT colon cancer.";
 RL Nature 396:699-703(1998).
 [2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.
 RC TISSUE=Prostate;
 RA MEDLINE=99253915; PubMed=10318773;
 RA Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
 RT "A newly identified member of tumor necrosis factor receptor
 RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
 RL J Biol. Chem. 274:13733-13736(1999).
 [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA MEDLINE=20122600; PubMed=10655513;
 RA Bai C., Connolly B., Metzger M.L., Hilliard C.A., Liu X., Sandig V.,
 RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
 RT "Overexpression of M68/Dc3 in human gastrointestinal tract tumors
 RT independent of gene amplification and its location in a four-gene
 RT cluster.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
 [4]
 RP SEQUENCE FROM N.A.
 RA Matthews L.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung, and Skin;
 RA MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Hopkins R.F., Zeeberg B., Buetow K.H., Scheeler C.F., Bhat N.K.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Staphenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.R.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Cantini P., Prange C.,
 RA Rana S.S., Loebellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulvik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,
 RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [6]
 RP FUNCTION: Decoy receptor for the cytotoxic ligands TNFSF4/LIGHT
 and TNFSF6/FasL. Protects against apoptosis.
 [7]
 RP SUBCELLULAR LOCATION: Secreted.
 [8]
 RP TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.
 Detected in adult stomach, spinal cord, lymph node, trachea,
 spleen, colon and lung. Highly expressed in several primary tumors
 from colon, stomach, rectum, esophagus and in SW480 colon
 carcinoma cells.
 [9]
 RP SIMILARITY: Contains 4 TNFR-Cys repeats.
 [10]
 RP This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation
 at the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC -----
 DR EMBL: AF104419; AAD03056.1; -
 DR EMBL: AF134340; AAD29688.1; -
 DR EMBL: AF217796; AAF35244.1; -
 DR EMBL: AF217793; AAF33685.1; -
 DR EMBL: AF217794; AAF33686.1; -
 DR EMBL: AL121845; CAC03668.1; -
 DR EMBL: BC017065; AAH17065.1; -
 DR EMBL: BC034349; AAH34349.1; -
 DR HSSP: O14763; 1D0G.
 DR Genew; HGNC:11921; TNFRSF6B.
 DR MIM; 603361; -
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0008189; F:apoptosis inhibitor activity; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0006916; P:anti-apoptosis; TAS.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 2.
 DR Receptor; Apoptosis; Glycoprotein; Repeat; Signal.
 KM SIGNAL 1 29
 FT CHAIN 30 300
 FT REPEAT 31 70 TUMOR NECROSIS FACTOR RECEPTOR
 FT REPEAT 72 113 SUPERFAMILY MEMBER 6B.
 FT REPEAT 115 150 TNFR-CYS 2.
 FT REPEAT 152 193 TNFR-CYS 3.
 FT REPEAT 195 232 TNFR-CYS 4.
 FT DISULFID 49 62 BY SIMILARITY.
 FT DISULFID 52 70 BY SIMILARITY.
 FT DISULFID 73 88 BY SIMILARITY.
 FT DISULFID 91 105 BY SIMILARITY.
 FT DISULFID 95 113 BY SIMILARITY.
 FT DISULFID 115 126 BY SIMILARITY.
 FT DISULFID 132 150 BY SIMILARITY.
 FT DISULFID 153 168 BY SIMILARITY.
 FT DISULFID 174 193 BY SIMILARITY.
 FT CARBOHYD 173 173 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 300 AA; 32679 MW; P0AEE33718449AF CRC64;
 Query Match 25.2%; Score 285.5; DB 1; Length 300;
 Best Local Similarity 36.0%; Pred. No. 1,5e-17;
 Matches 63; Conservative 18; Mismatches 77; Indels 17; Gaps 7;
 QY 25 EPQRICRCRPPGGVYSAKSRIRDTVCATCAENSVEHNNVLTICOLCEPCDPVMG-- 82
 DB 42 ETGERLVCAQCPGTFVORPCRDSPITCGCPPHHYQFNYL---ERCRVNLGGER 98
 QY 83 LEEIAPCTSKRKTQRCQCPGFC--AAWALFCTHCEILSDCPGTEAEIKDEVGKNNHCV 141
 DB 99 EEEAACHATNHRACRGTGFVAHAGFLE--H---ASCPPGA--GVIAPTPSQNTQCO 151
 QY 142 PCKAGHPONTSPSPARKCPHRCENQGLVEAPGTRQSDTTCKN---PLEPLPP 192
 DB 152 PCPPPTFSASSSSBQCQPHRNTALGLALNVGSSSHDTLCTSGTGFPLSTRVP 206
 RESULT 6
 TRIL MOUSE STANDARD; PRT; 625 AA.
 ID TRIL_MOUSE
 AC 035305; Q8VCT7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 11A precursor
 DE (Receptor activator of NF-kB) (Osteoclast differentiation factor
 DE Receptor) (ODFR).
 GN TNFRSF11A OR RANK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;

```

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=98032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Douglall W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
RA Gilbert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function.";
RL Nature 390:175-179 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carroll P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Helton E., Kettlem M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP FUNCTION.
RX MEDLINE=99097247; PubMed=9878548;
RA Nakagawa N., Kinoshita K., Yamaguchi K., Shima N., Yasuda H., Yano K.,
RA Morinaga T., Hirasaki K.;
RT "RANK is the essential signaling receptor for osteoclast
RT differentiation factor in osteoclastogenesis.";
RL Biochem. Biophys. Res. Commun. 253:395-400 (1998).
CC -!- FUNCTION: Receptor for TNFRSF11/RANKL/TRANCE/OPGL, essential for
CC interactions between osteoclastogenesis. Involved in the regulation of
CC interactions between T-cells and dendritic cells.
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN
CC TRABECULAR BONE, THYMUS, SMALL INTESTINE, LUNG, BRAIN AND KIDNEY.
CC WEAKLY EXPRESSED IN SPLEEN AND BONE MARROW.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF019046; AAB8610.1; -.
DR EMBL: BC019185; AAH19185.1; -.
DR HSSP: P25942; 1CDF.
DR MGD: MGI:1314891; Tnftrsf11a.
DR GO: GO:0007275; P:development; IMP.
DR GO: GO:0001503; P:ossification; IMP.
DR InterPro: IPR001368; TNFR_c6.
DR SMART: PF00020; TNFR_c6; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PSS0050; TNFR_NGFR_2; 1.

```

```

KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 625
FT FT
FT FT
FT DOMAIN 31 214
FT TRANSMEM 215 234
FT DOMAIN 235 625
FT REPEAT 35 69
FT REPEAT 72 113
FT REPEAT 115 152
FT REPEAT 155 195
FT DISULFID 35 47
FT DISULFID 48 61
FT DISULFID 51 69
FT DISULFID 72 87
FT DISULFID 93 113
FT DISULFID 115 128
FT DISULFID 134 152
FT CARBOHYD 106 106
FT CARBOHYD 175 175
FT COMFLICT 494 494
SQ SEQUENCE 625 AA; 66621 MW; F8C1872E99511DBE CRC64;

Query Match 25.0%; Score 283; DB 1; Length 625;
Best Local Similarity 32.6%; Pred. No. 5e-17;
Matches 60; Conservative 25; Mismatches 85; Indels 14; Gaps 4;

QY 4 QAVPPVASENGQTRDQKEKEYEPQHRICGRCRPGTVSAKCSIRDTVCATCENSYNE 63
DB 30 QVDPPTQGE-----RHYEHIGR-CGSRCEGKLSKCTPTSTVCLPCPDDEYLD 79
QY 64 HNNVLTICQLCRPDPPVGMEEIAPCTSKKTKGRCQCPGFMCAAMAECHTCELLSDCP 123
DB 80 TWMEDBCCLHKYCDACKALVAVDPGNHTAPRRACAGH--WNSDCECCRRNTECAP 136
QY 124 GTEAEIKDEVGKNNHCVPCKAGHPONTSSPSARCOPHTRCENOGIVAAFGTAQSDPTC 183
DB 137 GFGGQHPQLQNK-DTVCTPLGLGFSDFVSFTJCKKFWNTCTLLGKLEAHQGTIESDVVC 195
QY 184 KNPL 187
DB 196 SSSN 199

RESULT 7
TNRS_HUMAN STANDARD; PRT; 277 AA.
AC P25942; Q9BYU0;
DT 01-MAY-1992 (Rel. 22, Created)
DT 15-MAY-1992 (Rel. 22, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor
DE (CD40L receptor) (B-cell surface antigen CD40) (CDw40) (Bp50).
GN TNFRSF5 OR CD40.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM I).
RX MEDLINE=89356608; PubMed=2475341;
RA Stamenkovic I., Clark E.A., Seed B.;
RT "A B-lymphocyte activation molecule related to the nerve growth
RT factor receptor and induced by cytokines in carcinomas.";
RL EMBO J. 8:1403-1410 (1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM I).
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.B., Bridgeman A.M., Brown A.J.,
RA Buck D., Buttrill W.D., Butler A.P., Carder C., Carter N.P.,

```


RA Chapman J.C., Ciamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Cobby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahm D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leiva-Salho M.H., Levenson M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McCormachie L.J., McIlroy K., McMurtry A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,
RA Rice C.M., Ross M.T., Scott C.E., Senta H.K., Showkhen R., Sims S.,
RA Skuse C.D., Smith M.L., Soderlund C., Steward C.A., Sultson J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.,
RT "The DNA sequence and comparative analysis of human chromosome 20.",
RL Nature 414:865-871(2001).
RN [3]
RN SEQUENCE FROM N.A. (ISOFORM II).
RX MEDLINE=21117110; PubMed=11172023;
RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.,
RT "Regulation of CD40 function by its isoforms generated through
RT alternative splicing.",
RT Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).
RN [4]
RN SEQUENCE FROM N.A. (ISOFORM I).
RX TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Igoe L.N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.",
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RN INTERACTION WITH TRAF3.
RX MEDLINE=95184010; PubMed=7533327;
RA Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.,
RT "Involvement of CRAF, a relative of TRAF, in CD40 signaling.",
RT Science 267:1494-1498(1995).
RN [6]
RN INTERACTION WITH TRAF3.
RX MEDLINE=95129692; PubMed=7530216;
RA Sato T., Irie S., Reed J.C.,
RT "A novel member of the TRAF family of putative signal transducing
RT proteins binds to the cytosolic domain of CD40.",
RT FEBS Lett. 358:113-118(1995).
RN [7]
RN INTERACTION WITH TRAF1, TRAF2, TRAF3 AND TRAF5.
RX MEDLINE=98384149; PubMed=9718306;
RA Pullen S.S., Miller H.G., Everdeen D.S., Dang T.T., Crute J.J.,
RA Kehry M.R.,
RT "CD40-tumor necrosis factor receptor-associated factor (TRAF)
RT interactions: regulation of CD40 signaling through multiple TRAF

RT binding sites and TRAF hetero-oligomerization.",
RL Biochemistry 37:11836-11845(1998).
RN [8]
RN INTERACTION WITH TRAF5.
RX MEDLINE=98172745; PubMed=9511754;
RA Mitsuhashi S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
RA Otsuka M., Yamamoto T., Inoue J.-I.,
RT "Cloning and characterization of a cDNA encoding the human homolog of
RT tumor necrosis factor receptor-associated factor 5 (TRAF5).",
RL Gene 207:135-140(1998).
RN [9]
RN INTERACTION WITH TRAF6.
RX MEDLINE=98095703; PubMed=9432981;
RA Kashiwada M., Shirakata Y., Inoue J.-I., Nakano H., Okazaki K.,
RA Okamura K., Yamamoto T., Nagakura H., Takemori T.,
RT "Tumor necrosis factor receptor-associated factor 6 (TRAF6) stimulates
RT extracellular signal-regulated kinase (ERK) activity in CD40
RT signaling along a ras-independent pathway.",
RL J. Exp. Med. 187:237-244(1998).
RN [10]
RN 3D-STRUCTURE MODELING OF 24-144.
RX MEDLINE=97189482; PubMed=9037712;
RA Bajorek U., Arnulf A.,
RT "Construction and analysis of a detailed three-dimensional model of
RT the ligand binding domain of the human B cell receptor CD40.",
RL Proteins 27:59-70(1997).
RN [11]
RN 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
RX MEDLINE=9826353; PubMed=960517,
RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,
RA Zheng Z., Naismith J.H., Thomas D.,
RT "The role of polar interactions in the molecular recognition of CD40L
RT with its receptor CD40.",
RL Protein Sci. 7:1124-1135(1998).
RN [12]
RN X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 247-266 IN COMPLEX WITH
RN TRAF3.
RX MEDLINE=20442386; PubMed=10984535;
RA Ni C.Z., Welch K., Leo E., Chou C.K., Wu H., Reed J.C., Ely K.R.,
RT "Molecular basis for CD40 signaling mediated by TRAF3.",
RL Proc. Natl. Acad. Sci. U.S.A. 97:10395-10399(2000).
RN [13]
RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 178-195 IN COMPLEX WITH
RN TRAF3.
RX MEDLINE=22000222; PubMed=12005438;
RA Li C., Ni C.Z., Havert M.L., Cabezas E., He J., Kaiser D., Reed J.C.,
RA Satterthwaite A.C., Cheng G., Ely K.R.,
RT "Downstream regulator TRAF3 binds to the CD40 recognition site on
RT TRAF3.",
RL Structure 10:403-411(2002).
RN [14]
RN VARIANT HIGM3 ARG-83.
RX MEDLINE=21532985; PubMed=11675497;
RA Ferrai S., Gillani S., Insalaco A., Al-Chonaim A., Sorensen A.R.,
RA Loubser M., Avanzini M.A., Marconi M., Badolati R., Ugazio A.G.,
RA Levy Y., Catalan N., Durandy A., Tbakhi A., Notarangelo L.D.,
RT "Mutations of CD40 gene cause an autosomal recessive form of
RT immunodeficiency with hyper IgM.",
RT Proc. Natl. Acad. Sci. U.S.A. 98:12614-12619(2001).
RN [15]
RN FUNCTION: Receptor for TNFSF5/CD40L.
CC - FUNCTION: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
CC - SUBCELLULAR LOCATION: Type I membrane protein (isoform I);
CC secreted (isoform II).
CC - ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=I;
CC IsoId=P25942-1; Sequence=Displayed;
CC Name=II;
CC IsoId=P25942-2; Sequence=VSP_006472, VSP_006473;
CC - TISSUE SPECIFICITY: B-cells and in primary carcinomas.
CC - DISEASE: Defects in TNFRSF5 are the cause of hyper-IgM


```

CC immunodeficiency type 3 (HIGM3) [MIM:606843]. HIGM3 is an
CC autosomal recessive disorder which includes an inability of B
CC cells to undergo isotype switching, one of the final
CC differentiation steps in the humoral immune system, an inability
CC to mount an antibody-specific immune response, and a lack of
CC germinal center formation.
CC
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -1- DATABASE: NAME=PROT; NOTE=CD guide CD40 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; X60592; CAA43045.1; -
CC DR EMBL; AL035562; CAC17670.1; -
CC DR EMBL; AJ300189; CAC29424.1; -
CC DR EMBL; BC012419; AAH12419.1; -
CC DR PIR; S04460; A60771.
CC DR PDB; 1CDF; 01-APR-97.
CC DR PDB; 1FIL; 18-OCT-00.
CC DR PDB; 1LOA; 08-FEB-00.
CC DR PDB; 1CZ2; 26-SEP-01.
CC
CC
CC Query Match 24.5%; Score 278; DB 1; Length 277;
CC Best Local Similarity 35.0%; Pred. No. 6,1e-17;
CC Matches 62; Conservative 20; Mismatches 83; Indels 12; Gaps 5;
CC
CC QY 7 PPVASENQTGRDQKEXYEPQHRICSGRPPTVYSAKSGRIRDTVCATGNSYNHWN 66
CC DB 22 PPTA-----CR--EKQYLINSQ--CCSLCQPGKLVSDTCTEPTTECTLPGSESEFLDTWN 72
CC QY 67 YLTICQLCRPCDPMGLBEIAPCTSKKTKQCRCQPGMFCAMALECHTCLSDCPGTE 126
CC DB 73 RETHCHQHKYCDPMLGLRVQCKGISEDTTCTCEBGMHCTSEA--CSCVLSHSCSPGFG 130
CC QY 127 AELKDEVGKNNHCVPCSKAGHFOHTSSPASCOPHTRCENQGVLEAPGTAOSPTTC 183
CC DB 131 VK-QIATGVSDTICEPCPVGFSSVSAFKEKCHWTCTEKDLVVOAGINKIDVVC 186
CC
CC RESULT 8
CC ID TR11 HUMAN STANDARD; PRT; 616 AA.
CC AC G9Y6G6;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Tumor necrosis factor receptor superfamily member 11A precursor
CC DE (Receptor activator of NF-KB) (Osteoclast differentiation factor
CC DE receptor) (ODFPR).
CC GN TNFRSF11A OR RANK.
CC OS Homo sapiens (human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CC OX NCBI_TaxID=9606;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC TISSUE=Dendritic cell;
CC RA MEDLINE=98032977; PubMed=9367155;
CC RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
CC RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
CC RA Galibert L.;
CC RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
CC RT and dendritic-cell function.";
CC RL Nature 390:175-179 (1997).
CC FT [2]
CC RX MEDLINE=99097247; PubMed=9878548;
CC

```

```

RA Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,
RA Morinaga T., Higashio K.;
RA "RANK is the essential signaling receptor for osteoclast
RA differentiation factor in osteoclastogenesis.";
RA Biochem. Biophys. Res. Commun. 253:395-400 (1998).
RA
RA [3]
RA INTERACTION WITH TRAF1, TRAF2, TRAF3, TRAF5 AND TRAF6.
RA MEDLINE=98447691; PubMed=9774460;
RA Wong B.R., Jostien R., Lee S.Y., Vologodskaya M., Steinman R.M.,
RA Choi Y.;
RA "The TRAF family of signal transducers mediates NF-kappaB activation
RA by the TRANCE receptor.";
RA J. Biol. Chem. 273:28355-28359 (1998).
RA
RA [4]
RA VARIANT FEO LEU-LEU-CYS-ALA-LEU-LEU-21 INS. VARIANT PDB2
RA ALA-LEU-LEU-LEU-LEU-CYS-ALA-LEU-LEU-21 INS. AND VARIANT VAL-192.
RA MEDLINE=20082806; PubMed=10615125;
RA Hughes A.E., Ralston S.H., Marken J., Bell C., Macpherson H.,
RA Wallace R.G.H., van Hal W., Whyte M.P., Nakatsuka K., Hoyt L.,
RA Anderson D.M.;
RA "Mutations in TNFRSF11A, affecting the signal peptide of RANK, cause
RA familial expansile osteolysis.";
RA Nat. Genet. 24:45-48 (2000).
RA
RA -1- FUNCTION: Receptor for TNFRSF11/RANKL/TRANCE/OPGL; essential for
RA RANKL-mediated osteoclastogenesis. Involved in the regulation of
RA interactions between T-cells and dendritic cells.
RA -1- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
RA -1- SUBCELLULAR LOCATION: Type I membrane protein (potential).
RA -1- TISSUE SPECIFICITY: Ubiquitous expression with high levels in
RA skeletal muscle, thymus, liver, colon, small intestine and adrenal
RA gland.
RA
RA -1- DISEASE: Defects in TNFRSF11A are the cause of familial expansile
RA osteolysis (FEO) [MIM:174810]. FEO is a rare autosomal dominant
RA bone disorder characterized by focal areas of increased bone
RA remodelling. The osteolytic lesions develop usually in the long
RA bones during early adulthood. FEO is often associated with early
RA onset deafness and loss of dentition.
RA
RA -1- DISEASE: Defects in TNFRSF11A are a cause of Paget disease of bone
RA 2 (PDB2) [MIM:602080]; also known as familial Paget disease of
RA bone. PDB2 is a bone remodelling disorder with clinical
RA similarities to FEO. Unlike FEO, however, affected individuals
RA have involvement of the axial skeleton with lesions in the spine,
RA pelvis and skull.
RA
RA -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
RA
RA -----
RA This SWISS-PROT entry is copyright. It is produced through a collaboration
RA between the Swiss Institute of Bioinformatics and the EMBL outstation-
RA at the European Bioinformatics Institute. There are no restrictions on its
RA use by non-profit institutions as long as its content is in no way
RA modified and this statement is not removed. Usage by and for commercial
RA entities requires a license agreement (See http://www.isb-sib.ch/announce/
RA or send an email to license@isb-sib.ch).
RA
RA -----
RA EMBL; AF018253; AAB86809.1; -
RA HSSP; P25942; 1CDF.
RA DR Genew; HGNC:11908; TNFRSF11A.
RA DR MIM; 603499; -
RA DR MIM; 174810; -
RA DR MIM; 602080; -
RA DR GO; GO:0004872; F:receptor activity; TAS.
RA DR GO; GO:0007267; P:cell-cell signaling; TAS.
RA DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
RA DR GO; GO:0007165; P:signal transduction; TAS.
RA DR InterPro; IPR001368; TNFR_c6.
RA DR Pfam; PF00020; TNFR_c6; 4.
RA DR SMART; SM00208; TNFR_4.
RA DR PROSITE; PS00652; TNFR_NGFR_1; 1.
RA DR PROSITE; PS00500; TNFR_NGFR_2; 1.
RA KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
RA Disease mutation; Deafness.
RA FT SIGNAL 1 29
RA CHAIN 30 616
RA
RA POTENTIAL.
RA TUMOR NECROSIS FACTOR RECEPTOR
RA SUPERFAMILY MEMBER 11A.
RA

```

```

FT DOMAIN 30 212 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 213 233 POTENTIAL.
FT DOMAIN 234 616 CYTOPLASMIC (POTENTIAL).
FT REPEAT 34 68 TNFR-CYS 1.
FT REPEAT 71 112 TNFR-CYS 2.
FT REPEAT 114 151 TNFR-CYS 3.
FT REPEAT 154 194 TNFR-CYS 4.
FT DISULFID 34 46 BY SIMILARITY.
FT DISULFID 47 60 BY SIMILARITY.
FT DISULFID 50 68 BY SIMILARITY.
FT DISULFID 71 86 BY SIMILARITY.
FT DISULFID 92 112 BY SIMILARITY.
FT DISULFID 114 127 BY SIMILARITY.
FT DISULFID 133 151 BY SIMILARITY.
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 174 174 L-> LALLILCALL (in PDB3).
FT VARIANT 21 21 /Fttd=VAR_011516.
FT VARIANT 21 21 L-> LILCALL (in FEO).
FT VARIANT 21 21 /Fttd=VAR_011517.
FT VARIANT 21 21 A-> V.
FT VARIANT 192 192 /Fttd=VAR_011518.
FT SEQUENCE 616 AA; 66033 MM; E3DE9A7A08196F81 CRC64;
SQ
Query Match 24.4%; Score 277; DB 1; Length 616;
Best Local Similarity 31.7%; Pred. No. 1.6e-16;
Matches 60; Conservative 28; Mismatches 8; Indels 14; Gaps 4;
QY 4 QAVPPYASENQTCRDOEKYEYEPQHRICRCPPTGYVSACSRIRDTVCATCAENSUNE 63
DB 29 QIAPPCISE-----KHYEHLGR--CNKCEPGKVMSSKCTTSDVCLPCGPDXYLD 78
QY 64 HWNYLTTCQLCRPDPVWGLLEIAPCTSKRTQCRQCGMCAMALECTHCELLSDCP 123
DB 79 SWNEEDKCLHKVCTGKALVAVAGNSTPRRCCTVGYH---WSQDCECCRRNTECAP 135
QY 124 GTEAELEKQEVKGNHCVPCAKGHQONTSSPARCQPHTRCENQGLVEAPGTASDPTTC 183
DB 136 GLGAGHPVLQVLRN-DIVCKPCLAGFSDAFSSTDKCRPWNCTFLGKRVHHGTESDAVC 194
QY 184 KNPLEPLPP 192
DB 195 SSSUPARKP 203

```

```

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U57745; AAC48710.1; -.
DR HSPB; P25942; ICDP.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4. NGR_1; 1.
DR PROSITE; PS00652; TNFR_NGR_1; 1.
DR PROSITE; PS50050; TNFR_NGR_2; 1.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 19
FT CHAIN 20 >269
FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 194 215 POTENTIAL.
FT DOMAIN 216 >269 CYTOPLASMIC (POTENTIAL).
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 103 TNFR-CYS 2.
FT REPEAT 104 144 TNFR-CYS 3.
FT REPEAT 145 187 TNFR-CYS 4.
FT DISULFID 26 37 BY SIMILARITY.
FT DISULFID 38 51 BY SIMILARITY.
FT DISULFID 41 59 BY SIMILARITY.
FT DISULFID 62 77 BY SIMILARITY.
FT DISULFID 83 103 BY SIMILARITY.
FT DISULFID 105 119 BY SIMILARITY.
FT DISULFID 111 116 BY SIMILARITY.
FT DISULFID 125 143 BY SIMILARITY.
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 269
SQ SEQUENCE 269 AA; 29983 MM; 746903F30F95F387 CRC64;
Query Match 22.2%; Score 251.5; DB 1; Length 269;
Best Local Similarity 33.1%; Pred. No. 1.1e-14;
Matches 55; Conservative 21; Mismatches 81; Indels 9; Gaps 4;
QY 20 EKERYEPQHRICRCPPTGYVSACSRIRDTVCATCAENSUNEHWNYLTTCQLCRPDP 79
DB 28 EKQY--PVNSLCQDLCPFGQKLVNDCTEVSRTKTCQSGKGEPLSTNREKXCHEHYCNP 85
QY 80 VMGLEIAPCTSKRTQCRQCGMFCAMALECTHCELLSDCPGTEAELEKDEVGKG--N 137
DB 86 NIGLRIGSEGLNDITLCVYBGQHTSHT--CEECTHSLCLPFGVK---QIATGLLD 140
QY 138 NHCVCCKAGHFQNTSSPARCQPHTRCENQGLVEAPGTASDPTTC 183
DB 141 TVCEPCPLGPFSSNVSAFEKCHRWTSCEKRGIVGEQVGTNKTDVVC 186

```

```

RESULT 10
TNRS_MOUSE
ID TNRS_MOUSE STANDARD; PRT; 289 AA.
AC P27512; Q99NE0; Q99NE1; Q99NE2; Q99NE3;
DT 01-AUG-1992 (Rel. 23. Created)
DT 01-OCT-1996 (Rel. 34. Last sequence update)
DT 10-OCT-2003 (Rel. 42. Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor
DE (CD40L receptor) (B-cell surface antigen CD40) (Bp50) (CDw40).
GN TNFRSF5 OR CD40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
NCBI_TaxID=10090;

```


ID	TI1B MOUSE	STANDARD;	PRT;	401 AA.
AC	008712;	070202;		
DT	28-FEB-2003	(Rel. 41, Created)		
DT	28-FEB-2003	(Rel. 41, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Tumor necrosis factor receptor superfamily member 11B precursor			
DE	(osteoprotegerin) (osteoclastogenesis inhibitory factor).			
GN	TNFRSF11B OR OPG OR OCIF.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId:10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BALB/c; TISSUE=Kidney;			
RX	MEDLINE=9762071; PubMed=9108485;			
RA	Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,			
RA	Liethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,			
RA	DeRose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,			
RA	Davy E., Bucy N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,			
RA	Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,			
RA	Suggs S., Boyle W.J.,			
RT	"osteoprotegerin: a novel secreted protein involved in the regulation			
RT	of bone density.";			
RL	Cell 89:309-319(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND VARIANTS PRO-138; ARG-161; ASP-165; ALA-288			
RP	AND ARG-296			
RC	STRAIN=129/Ola, and NIH Swiss; TISSUE=Fibroblast;			
RX	MEDLINE=99382527; PubMed=9714833;			
RA	Mituno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,			
RA	Higashio K.;			
RT	"Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)			
RT	gene and its expression in embryogenesis.";			
RL	Gene 215:339-343(1998).			
RN	[3]			
RP	FUNCTION.			
RP	MEDLINE=21060987; PubMed=10952716;			
RA	Min H., Moroy S., Sarosi I., Dunstan C.R., Capparelli C., Scully S.,			
RA	Van G., Kaufman S., Kostenuik P.J., Lacey D.L., Boyle W.J.,			
RA	Simonet W.S.;			
RT	"osteoprotegerin reverses osteoporosis by inhibiting endosteal			
RT	osteoclasts and prevents vascular calcification by blocking a process			
RT	resembling osteoclastogenesis.";			
RL	J. Exp. Med. 192:1463-1474(2000).			
CC	-1- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes			
CC	its function in osteoclastogenesis. Inhibits the activation of			
CC	osteoclasts and promotes osteoclast apoptosis in vitro. Bone			
CC	homeostasis seems to depend on the local RANKL/OPG ratio. May also			
CC	play a role in preventing arterial calcification. May act as decoy			
CC	receptor for TRAIL and protect against apoptosis. TRAIL binding			
CC	blocks the inhibition of osteoclastogenesis.			
CC	-1- SUBUNIT: Homodimer.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach,			
CC	intestines and calvaria. Highly expressed in decidua and placenta,			
CC	and in embryo.			
CC	-1- DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7,			
CC	whereas expression decreases at day 11 and increases from day 15			
CC	to 17. On day 15 found in developing bone primordia,			
CC	brachiocephalic artery and ductus arteriosus, left main bronchus,			
CC	abdominal aorta and midgut.			
CC	-1- INDUCTION: Upregulated by TGF-beta and estrogens. Downregulated by			
CC	1,25-dihydroxyvitamin D3 and parathyroid hormone.			
CC	-1- SIMILARITY: Contains 4 TNFR-Cys repeats.			
CC	-1- SIMILARITY: Contains 2 death domains.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			

DB	SEQUENCE	401 AA, 45923 MW, CAA6102DB312470 CRC64;	Score 242.5; DB 1; Length 401; Best Local Similarity 29.6%; Pred. No. 9, 4e-14; Matches 50; Conservative 25; Mismatches 83; Indels 11; Gaps 5
QY	23 YIEPQ--HRIICSRCPGGTYVAACKSRIDYCATCAENSYEMHMYLTICQLCRP-CDP		79
DB	30 HYDPFEGHLLDCKCAPGTYLLKQHCVRKRTLCVPCPDHSYDMSWHTSDCEVCYCSFVCKE		89
QY	80 VNGLEIACCTSKRKTCQRCQPGMFCAMALAECTHCELLSDCPGTEALKDEVGKGNH		139
DB	90 LOSVKQ--ECNRTINNVCECEBRY-----LIEFELIKRSRCPGS--GVYQAGTPERRNV		141
QY	140 CVPCCKGHPQNTSSPSARCPHTRCENQGLVEAAPSTAQSDTTCKNPLE		188
DB	142 CKCKCPGFGFSSGETSSKAPCIKHINNGTFFGLLIQKGNATHDNCGNRE		190

RESULT 12
 T11B HUMAN STANDARD; FRT; 401 AA.
 ID T11B_HUMAN STANDARD; FRT; 401 AA.
 AC 000300; 060236; Q9UHP4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 11B precursor
 GN TNFRSF11B OR OPG OR OCIF.
 OS (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=97262071; PubMed=9108485;
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
 RA Luehly R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
 RA Suggs S., Boyle W.J.;
 RT "Osteoprotegerin: a novel secreted protein involved in the regulation
 RT of bone density.";
 RL Cell 89:309-319(1997).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung cancer;
 RX MEDLINE=98151033; PubMed=9492069;
 RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
 RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
 RA Tsuda E., Morinaga T., Higashio K.;
 RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
 RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
 RT osteoclastogenesis in vitro.";
 RL Endocrinology 139:1329-1337(1998).
 [3]
 RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
 RC TISSUE=Placenta;
 RX MEDLINE=9831569; PubMed=9688283;
 RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
 RT "Cloning and characterization of the gene encoding human
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";
 RL Eur. J. Biochem. 254:685-691(1998).
 [4]
 RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schlier G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh L.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.D., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., Mcwan P.J., McKernan K.J., Malek J.A., Gauratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
 RA Villalón D.K., Muray D.M., Sodegren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Trichman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Groomwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Maita M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [5]

RP SEQUENCE OF 22-36 AND 378-401.
 RX MEDLINE=98238645; PubMed=9571159;
 RA Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,
 RA Morinaga T., Tsuda E., Higashio K.;
 RT "Characterization of monomeric and homodimeric forms of
 RT osteoclastogenesis inhibitory factor.";
 RL Biochem. Biophys. Res. Commun. 245:382-387(1998).
 [6]
 RP SEQUENCE OF 22-393 FROM N.A.
 RC TISSUE=Placenta;
 RT He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
 RL Acta Biochim. Biophys. Sin. 31:680-684(1999).
 [7]
 RP SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.
 RX MEDLINE=97312536; PubMed=9168977;
 RA Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,
 RA Morinaga T., Higashio K.;
 RT "Isolation of a novel cytokine from human fibroblasts that
 RT specifically inhibits osteoclastogenesis.";
 RL Biochem. Biophys. Res. Commun. 234:137-142(1997).
 [8]
 RP TRAIL BINDING.
 RX MEDLINE=98269100; PubMed=9603945;
 RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C.,
 RA Dul E., Appelbaum E.R., Richman C., DiPrinzio R., Dadds R.A.,
 RA James I.E., Rosenberg M., Lee J.C., Young P.R.;
 RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";
 RL J. Biol. Chem. 273:14363-14367(1998).
 [9]
 RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
 RX MEDLINE=98148058; PubMed=9478964;
 RA Yamaguchi K., Kinoshita M., Goto M., Kobayashi F., Tsuda E.,
 RA Morinaga T., Higashio K.;
 RT "Characterization of structural domains of human osteoclastogenesis
 RT inhibitory factor.";
 RL J. Biol. Chem. 273:5117-5123(1998).
 [10]
 RP REVIEW.
 RX MEDLINE=21395914; PubMed=11505389;
 RA Hofbauer L.C., Neuberger A., Heutelder A.E.;
 RT "Receptor activator of nuclear factor-kappaB ligand and
 RT osteoprotegerin: potential implications for the pathogenesis and
 RT treatment of malignant bone diseases.";
 RL Cancer 92:460-470(2001).
 CC -1- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
 CC its function in osteoclastogenesis. Inhibits the activation of
 CC osteoclasts and promotes osteoclast apoptosis in vitro. Bone
 CC homeostasis seems to depend on the local RANKL/OPG ratio. May also
 CC play a role in preventing arterial calcification. TRAIL binding
 CC blocks the inhibition of osteoclastogenesis.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney,
 CC liver, spleen, thymus, prostate, ovary, small intestine, thyroid,
 CC lymph node, trachea, adrenal gland, testis, and bone marrow.
 CC detected at very low levels in brain, placenta and skeletal
 CC muscle. Highly expressed in fetal kidney, liver and lung.
 CC -1- INDUCTION: Upregulated by increasing calcium-concentration in the
 CC medium and estrogens. Downregulated by glucocorticoids.
 CC -1- PTM: N-glycosylated. Contains static acid residues.
 CC -1- PTM: The N-terminus is blocked.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- SIMILARITY: Contains 2 death domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

FT DISULFID 107 118 BY SIMILARITY.
 FT DISULFID 124 142 BY SIMILARITY.
 FT DISULFID 145 160 BY SIMILARITY.
 FT DISULFID 166 185 BY SIMILARITY.
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 401 AA: FE6A31FD4E573A CRC64;
 Query Match 20.8%; Score 235.5; DB 1; Length 401;
 Best Local Similarity 29.6%; Pred. No. 3.7e-13;
 Matches 50; Conservative 24; Mismatches 84; Indels 11; Gaps 5;
 QY 23 YYPEP--HRICCSRPCTGYSAKSRIRDTVCATCAENSNEHNNYITICQLCRP--CDP 79
 DB 30 HYDEPGRQLLCDCRACPGTYLKQCTVRRKTLVCPDPYSTDSWHTSDECVYCSPVCKE 89
 QY 80 VMGLEIAPCTSKRKTQCRCPGMFCAMALECTHCELLSDCPGTETELKDEYKGNH 139
 DB 90 LQTVKQ--ECNRTNRRVCEEGRY----LELEPLKHSRCPQL--GVLDAGTPERTV 141
 QY 140 CVPCKAGHPONTSSPARCOPHTRCENQGLVEAPGTAQSDPTCKNPLE 188
 DB 142 CKRCPDGFFSGSTSSKAPCRKHTNCSSILGLLLQKNAHTHNVCSGNRE 190
 RESULT 14
 ID TR14 HUMAN STANDARD; PRT; 283 AA.
 AC Q92956; Q8WXK1; Q96J31; Q9UM65;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 14 precursor
 DE (Herpesvirus entry mediator A) (Tumor necrosis factor receptor-like 2)
 DE (TR2).
 GN TNFRSF14 OR HVEM OR HVFA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cervical adenocarcinoma;
 RX MEDLINE=97053782; PubMed=898196;
 RA Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
 RT "Herpes simplex virus-1 entry into cells mediated by a novel member of
 the TNF/NGF receptor family.";
 RL Cell 87:427-436(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97306336; PubMed=9162061;
 RA Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J.,
 RA Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,
 RA Porter T.G., Tumbah A., Young P.R.;
 RT "A newly identified member of the tumor necrosis factor receptor
 superfamily with a wide tissue distribution and involvement in
 lymphocyte activation.";
 RL J. Biol. Chem. 272:14272-14276(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Zhang W., Man T., Cao X.;
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANTS ARG-17 AND ILE-241.
 RX MEDLINE=21629477; PubMed=11756979;
 RA Struyf F., Posavac C.M., Keyaerts E., Van Raest M., Corey L.,
 RA Spear P.G.;
 RT "Search for polymorphisms in the genes for herpesvirus entry mediator,
 RT Nectin-1, and Nectin-2 in immune seronegative individuals.";
 RL J. Infect. Dis. 185:36-44(2002).
 RN [5]

RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.D., Fellings F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Blat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Ditchenko L., Marusina K., Farmer A., Rubin J., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Roha S.S., Loguelfano N.A., Peters G.J., Adamson R.D., Mollath S.J.,
 RA Bask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP INTERACTION WITH TRAF2 AND TRAF5.
 RX MEDLINE=97298041; PubMed=9153189;
 RA Hsu H., Solovoyev I., Colombo A., Elliott R., Kelley M., Boyle W.J.;
 RT "ATAR, a novel tumor necrosis factor receptor family member, signals
 RT through TRAF2 and TRAF5.";
 RL J. Biol. Chem. 272:13471-13474(1997).
 RN [7]
 RP INTERACTION WITH TRAF3 AND TRAF5.
 RX MEDLINE=97306297; PubMed=9162022;
 RA Marsters S.A., Ayres T.M., Skubatch M., Gray C.L., Rothe M.,
 RA Ashkenazi A.;
 RT "Herpesvirus entry mediator, a member of the tumor necrosis factor
 RT receptor (TNFR) family, interacts with members of the TNFR-associated
 RT factor family and activates the transcription factors NF-kappaB and
 RT AP-1.";
 RL J. Biol. Chem. 272:14029-14032(1997).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 39-200.
 RX MEDLINE=21403268; PubMed=11511370;
 RA Carli A., Willis S.H., Whitbeck J.C., Krummenacher C., Cohen G.H.,
 RA Eisenberg R.J., Wiley D.C.;
 RT "Herpes simplex virus glycoprotein D bound to the human receptor
 RT Hvea-1.";
 RL Mol. Cell 8:169-179(2001).
 CC -I- FUNCTION: Receptor for TNFRSF14/LIGHT and homotrimeric
 CC TNFRSF14/lymphotoxin-alpha. Involved in lymphocyte activation. Plays
 CC an important role in HSV pathogenesis because it enhanced the
 CC entry of several wildtype HSV strains of both serotypes into CHO
 CC cells, and mediated HSV entry into activated human T cells.
 CC -I- SUBUNIT: Interacts with TRAF2, TRAF3 and TRAF5.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
 CC -I- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION
 CC IN LUNG, SPLEEN, AND THYMUS.
 CC -I- SIMILARITY: Contains 3 TNFR-Cys repeats.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, U70321; AAB58354.1; -
 CC EMBL, U81232; AAD00505.1; -
 CC EMBL, AF153978; AAF75588.1; -
 CC EMBL, AF373877; AAL47717.1; -
 CC EMBL, AF373878; AAL47718.1; -
 CC EMBL, BC002794; AAO2794.1; -

CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; AF068868; AAC34583.1; -
DR EMBL; AL096801; CAB75692.1; -
DR EMBL; BC017730; AAH17730.1; -
DR EMBL; BC010241; AAH10241.1; ALT_INIT.
DR HSSP; O14763; IDOG.
DR Genew; HGNC:13469; TNFRSF21.
DR MIM; 605732; -
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00531; death; 1.
DR SMART; SM00020; TNFR_C6; 4.
DR SMART; SM00005; DEATH; 1.
DR PROSITE; PS50017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
DR Receptor; Apoptosis; Transmembrane; Repeat; Signal.
FT SIGNAL 1 41 POTENTIAL.
FT CHAIN 42 655 TUMOR NECROSIS FACTOR RECEPTOR
FT FT 42 655 SUPERFAMILY MEMBER 21.
FT TRANSMEM 350 370 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 371 655 POTENTIAL.
FT DOMAIN 415 498 CYTOPLASMIC (POTENTIAL).
FT REPEAT 50 88 DEATH.
FT REPEAT 90 131 TNFR-CYS 1.
FT REPEAT 133 167 TNFR-CYS 2.
FT REPEAT 170 211 TNFR-CYS 3.
FT DISULFID 67 80 TNFR-CYS 4.
FT DISULFID 70 88 BY SIMILARITY.
FT DISULFID 91 106 BY SIMILARITY.
FT DISULFID 109 123 BY SIMILARITY.
FT DISULFID 113 131 BY SIMILARITY.
FT DISULFID 133 144 BY SIMILARITY.
FT DISULFID 150 168 BY SIMILARITY.
FT DISULFID 171 186 BY SIMILARITY.
FT DISULFID 192 211 BY SIMILARITY.
FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 655 AA; 71844 MW; 48939391C4852A33 CRC64;

Query Match Best Local Similarity 20.2%; Score 228.5; DB 1; Length 655;
Matches 56; Conservative 23; Mismatches 65; Indels 37; Gaps 8;

QY 30 ICCSRCPPTGVYSAKSRIRDTVCATCAENSYHEHNNYLLICQLC-RPCDPVAGLEELAP 88
Db 65 LITCDKCPAGTYVSEHCTNTSLKVCSSCPVGTFRHENGIEKCHDCQPC-PWMTBKL-P 122
QY 89 CTSKRKTQCRQCPGMF-----CAWALBCTHCEHLSDCP-----PSTEAEIKDEVGKG 136
Db 123 CAALTDRECTCPFGMFGSNATCAPHTV-----CPVGMGVRRKGTETE----- 164
QY 137 NNHCVPCXKGFHONTSPSARCPHRCENOGIVEAPGTAOSDTTCKNPLEPLPEMSG 196
Db 165 DVRCXQCARGTSPDVSSVWCKKAYTDLSONLVVIKPGTKETDNCVT---LTFSSSS 220
QY 197 T 197
Db 221 T 221

Search completed: August 27, 2004, 21:08:21
Job time : 24 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 27, 2004, 21:05:51 ; Search time 32 Seconds

(without alignments)
317,822 Million cell updates/sec

Title: US-09-626-219-1

Perfect score: 1133

Sequence: 1 SQOAVPVASENQTCDQF.....QSDTTCKNPLELPKMSGT 197

Scoring table: BLASTSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/2/1aa/5A COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B COMB.pep:*
3: /cgn2_6/prodata/2/1aa/5A COMB.pep:*
4: /cgn2_6/prodata/2/1aa/5B COMB.pep:*
5: /cgn2_6/prodata/2/1aa/5A COMB.pep:*
6: /cgn2_6/prodata/2/1aa/5A COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1133	100.0	197	2	US-08-505-606-1
2	1133	100.0	197	4	US-09-000-166-1
3	1133	100.0	197	4	US-09-303-262-1
4	987	87.1	170	4	US-08-828-683A-14
5	981	86.6	170	4	US-09-523-323-57
6	771	68.0	415	3	US-09-006-353A-6
7	771	68.0	415	3	US-09-573-986-6
8	456	40.2	77	3	US-08-866-545-3
9	456	40.2	77	3	US-09-627-775-3
10	305	26.9	227	3	US-08-974-023-48
11	305	26.9	227	3	US-08-795-445A-48
12	305	26.9	227	3	US-08-795-447A-48
13	305	26.9	227	3	US-08-974-186-48
14	305	26.9	227	3	US-08-795-446B-48
15	305	26.9	227	3	US-08-706-945D-134
16	305	26.9	227	4	US-08-577-788C-48
17	305	26.9	235	4	US-09-326-394-4
18	305	26.9	235	4	US-09-580-235-2
19	305	26.9	235	4	US-09-580-235-8
20	305	26.9	235	4	US-09-580-181-2
21	305	26.9	235	4	US-09-580-181-8
22	305	26.9	235	4	US-09-102-530-2
23	305	26.9	235	4	US-09-102-530-8
24	305	26.9	257	4	US-09-579-845-10
25	305	26.9	461	1	US-08-385-229-2
26	305	26.9	461	2	US-08-650-000-2
27	305	26.9	461	3	US-09-042-785A-7

28	305	26.9	461	3	US-08-477-347-3	Sequence 3, Appli
29	305	26.9	461	3	US-09-006-353A-4	Sequence 4, Appli
30	305	26.9	461	3	US-08-476-862-2	Sequence 2, Appli
31	305	26.9	461	4	US-09-573-986-4	Sequence 4, Appli
32	305	26.9	461	4	US-08-406-824A-2	Sequence 2, Appli
33	305	26.9	461	4	US-09-800-909-2	Sequence 2, Appli
34	305	26.9	461	4	US-09-758-124-2	Sequence 2, Appli
35	305	26.9	461	4	US-09-800-908-3	Sequence 3, Appli
36	305	26.9	461	6	5395760-2	Patent No. 5395760
37	305	26.9	486	1	US-08-243-010-1	Sequence 1, Appli
38	305	26.9	518	1	US-08-385-229-4	Sequence 4, Appli
39	305	26.9	518	4	US-09-579-845-1	Sequence 1, Appli
40	305	26.9	518	4	US-09-579-845-3	Sequence 1, Appli
41	304	26.8	235	4	US-09-580-235-4	Sequence 4, Appli
42	304	26.8	235	4	US-09-580-235-6	Sequence 4, Appli
43	304	26.8	235	4	US-09-580-181-4	Sequence 4, Appli
44	304	26.8	235	4	US-09-580-181-6	Sequence 6, Appli
45	304	26.8	235	4	US-09-102-530-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-505-606-1
Sequence 1, Application US/08505606
Patent No. 5925351
GENERAL INFORMATION:
APPLICANT: BROMING, Jeffrey L.
APPLICANT: BROMING, Christopher D.
APPLICANT: HOCHMAN, Paula S.
TITLE OF INVENTION: SOLUBLE LYMPHOTOXIN-BETA RECEPTORS AND
TITLE OF INVENTION: ANTI-LYMPHOTOXIN RECEPTOR AND LIGAND ANTIBODIES AS
TITLE OF INVENTION: THERAPEUTIC AGENTS FOR THE TREATMENT OF IMMUNOLOGICAL
DISEASE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr.
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,606
FILING DATE: 21-JUL-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378,968
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B191
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-505-606-1
Query Match 100.0%; Score 1133; DB 2; Length 197;

Best Local Similarity 100.0%; Pred. No. 2.5e-99;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGPQAVPPYASSENQTCRDQEKYEYEPQHRICCSRCPGTYVSAAKSRIRDTVCATCAENS 60
Db 1 SGPQAVPPYASSENQTCRDQEKYEYEPQHRICCSRCPGTYVSAAKSRIRDTVCATCAENS 60
QY 61 YNEHNNVLTICQLCRPCDPVWGLEIAFCTSKRTQCGQGMFCAMALECTHCELLSD 120
Db 61 YNEHNNVLTICQLCRPCDPVWGLEIAFCTSKRTQCGQGMFCAMALECTHCELLSD 120
QY 121 CPPTGAEALKDEVKGNHNCVPCAKGHFQNTSSPSARCOPTHRCENOGUVEAAPGTAQSD 180
Db 121 CPPTGAEALKDEVKGNHNCVPCAKGHFQNTSSPSARCOPTHRCENOGUVEAAPGTAQSD 180
QY 181 TTCKNPLEPLPPEMSGT 197
Db 181 TTCKNPLEPLPPEMSGT 197

RESULT 2

US-09-000-166-1
; Sequence 1, Application US/09000166A
; Patent No. 6403087
; GENERAL INFORMATION:
; APPLICANT: BROWNING, et al.
; TITLE OF INVENTION: Soluble Lymphotoxin-B Receptors and Anti-Lymphotoxin
; TITLE OF INVENTION: Receptor and Ligand Antibodies, as Therapeutic Agents
; TITLE OF INVENTION: for the Treatment of Immunological Disease.
; FILE REFERENCE: B191
; CURRENT APPLICATION NUMBER: US/09/000,166A
; CURRENT FILING DATE: 1998-06-08
; EARLIER APPLICATION NUMBER: PCT/US96/12010
; EARLIER FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-000-166-1

Query Match 100.0%; Score 1133; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.5e-99;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGPQAVPPYASSENQTCRDQEKYEYEPQHRICCSRCPGTYVSAAKSRIRDTVCATCAENS 60
Db 1 SGPQAVPPYASSENQTCRDQEKYEYEPQHRICCSRCPGTYVSAAKSRIRDTVCATCAENS 60
QY 61 YNEHNNVLTICQLCRPCDPVWGLEIAFCTSKRTQCGQGMFCAMALECTHCELLSD 120
Db 61 YNEHNNVLTICQLCRPCDPVWGLEIAFCTSKRTQCGQGMFCAMALECTHCELLSD 120
QY 121 CPPTGAEALKDEVKGNHNCVPCAKGHFQNTSSPSARCOPTHRCENOGUVEAAPGTAQSD 180
Db 121 CPPTGAEALKDEVKGNHNCVPCAKGHFQNTSSPSARCOPTHRCENOGUVEAAPGTAQSD 180
QY 181 TTCKNPLEPLPPEMSGT 197
Db 181 TTCKNPLEPLPPEMSGT 197

RESULT 3

US-09-303-262-1
; Sequence 1, Application US/09303262
; Patent No. 6669941
; GENERAL INFORMATION:
; APPLICANT: BROWNING, Jeffrey L.
; BENJAMIN, Christopher D.
; HOCHMAN, Paula S.
; TITLE OF INVENTION: SOLUBLE LYMPHOTOXIN-BETA RECEPTORS AND
; ANTI-LYMPHOTOXIN RECEPTOR AND LIGAND ANTIBODIES AS

TERAPEUTIC AGENTS FOR THE TREATMENT OF IMMUNOLOGICAL
DISEASE

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr.

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/303,262

FILING DATE: 30-Apr-1999

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/505,606

FILING DATE: 21-Jul-1995

APPLICATION NUMBER: US 08/378,968

FILING DATE: 26-Jan-1995

ATTORNEY/AGENT INFORMATION:

NAME: HALEY, Jr., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: B191

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090

TELEX: 14-8367

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 197 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Query Match 100.0%; Score 1133; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.5e-99;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGPQAVPPYASSENQTCRDQEKYEYEPQHRICCSRCPGTYVSAAKSRIRDTVCATCAENS 60
Db 1 SGPQAVPPYASSENQTCRDQEKYEYEPQHRICCSRCPGTYVSAAKSRIRDTVCATCAENS 60
QY 61 YNEHNNVLTICQLCRPCDPVWGLEIAFCTSKRTQCGQGMFCAMALECTHCELLSD 120
Db 61 YNEHNNVLTICQLCRPCDPVWGLEIAFCTSKRTQCGQGMFCAMALECTHCELLSD 120
QY 121 CPPTGAEALKDEVKGNHNCVPCAKGHFQNTSSPSARCOPTHRCENOGUVEAAPGTAQSD 180
Db 121 CPPTGAEALKDEVKGNHNCVPCAKGHFQNTSSPSARCOPTHRCENOGUVEAAPGTAQSD 180
QY 181 TTCKNPLEPLPPEMSGT 197
Db 181 TTCKNPLEPLPPEMSGT 197

RESULT 4

US-08-828-683A-14
; Sequence 14, Application US/08828683A
; Patent No. 6469144
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 L1 AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.

```
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Winpatin (Genentech)
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/828,683A
/ FILING DATE: 31-Mar-1997
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/625328
/ FILING DATE: 1-Apr-1996
/ APPLICATION NUMBER: 08/710802
/ FILING DATE: 23-Sep-1996
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Marschang, Diane L.
/ REGISTRATION NUMBER: 35,600
/ REFERENCE/DOCKET NUMBER: P1007P1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-5416
/ TELEFAX: 650/952-9881
/
/ INFORMATION FOR SEQ ID NO: 14:
/
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 170 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-08-828-683A-14

Query Match      87.1%; Score 987; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-85;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TCDDQKEYEYEPQHRICCSRCPGTYVSACSRIRPTVCATCAENSYNEHMYLTTCQLC 74
DB 1 TCDDQKEYEYEPQHRICCSRCPGTYVSACSRIRPTVCATCAENSYNEHMYLTTCQLC 60

QY 75 RCPDPMGLIEIAPCTSKRTQCRQCPGMFCAMALECTHCELLSDCPPTAELELDEVG 134
DB 61 RCPDPMGLIEIAPCTSKRTQCRQCPGMFCAMALECTHCELLSDCPPTAELELDEVG 120

QY 135 KANNHCVPKAGHFQNTSSPSARQCPHTRCENQGLVEAARPTAQSPTTCK 184
DB 121 KANNHCVPKAGHFQNTSSPSARQCPHTRCENQGLVEAARPTAQSPTTCK 170

RESULT 5
US-09-523-323-57
/ Sequence 57, Application US/09523323
/ Patent No. 6635743
/ GENERAL INFORMATION:
/ APPLICANT: Ebner, Reinhard
/ APPLICANT: Yu, Guo-Liang
/ APPLICANT: Ruben, Steven M.
/ APPLICANT: Ulrich, Stephen
/ APPLICANT: Zhai, Yifan
/ TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
/ FILE REFERENCE: 1488,065000C
/ CURRENT APPLICATION NUMBER: US/09/523,323
/ EARLIER FILING DATE: 2000-03-10
/ EARLIER APPLICATION NUMBER: 60/168,380
/ EARLIER FILING DATE: 1999-12-02
/ EARLIER APPLICATION NUMBER: 60/148,326
/ EARLIER FILING DATE: 1999-08-11
/ EARLIER APPLICATION NUMBER: 60/142,657
/ EARLIER FILING DATE: 1999-07-06
/ EARLIER APPLICATION NUMBER: 60/137,457
/ EARLIER FILING DATE: 1999-06-04
```

```
/ EARLIER APPLICATION NUMBER: 60/124,041
/ EARLIER FILING DATE: 1999-03-11
/ EARLIER APPLICATION NUMBER: 09/252,656
/ EARLIER FILING DATE: 1999-02-19
/ EARLIER APPLICATION NUMBER: 60/075,409
/ EARLIER FILING DATE: 1998-02-20
/ EARLIER APPLICATION NUMBER: 09/027,287
/ EARLIER FILING DATE: 1998-02-20
/ EARLIER APPLICATION NUMBER: 09/003,886
/ EARLIER FILING DATE: 1998-01-07
/ EARLIER APPLICATION NUMBER: 08/822,953
/ EARLIER FILING DATE: 1997-03-21
/ EARLIER APPLICATION NUMBER: 60/013,923
/ EARLIER FILING DATE: 1996-03-22
/ EARLIER APPLICATION NUMBER: 60/030,157
/ EARLIER FILING DATE: 1996-10-31
/ NUMBER OF SEQ ID NOS: 70
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 57
/ LENGTH: 170
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: (7)
/ OTHER INFORMATION: May be any amino acid
US-09-523-323-57

Query Match      86.6%; Score 981; DB 4; Length 170;
Best Local Similarity 99.4%; Pred. No. 4.3e-85;
Matches 169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 TCDDQKEYEYEPQHRICCSRCPGTYVSACSRIRPTVCATCAENSYNEHMYLTTCQLC 74
DB 1 TCDDQKEYEYEPQHRICCSRCPGTYVSACSRIRPTVCATCAENSYNEHMYLTTCQLC 60

QY 75 RCPDPMGLIEIAPCTSKRTQCRQCPGMFCAMALECTHCELLSDCPPTAELELDEVG 134
DB 61 RCPDPMGLIEIAPCTSKRTQCRQCPGMFCAMALECTHCELLSDCPPTAELELDEVG 120

QY 135 KANNHCVPKAGHFQNTSSPSARQCPHTRCENQGLVEAARPTAQSPTTCK 184
DB 121 KANNHCVPKAGHFQNTSSPSARQCPHTRCENQGLVEAARPTAQSPTTCK 170

RESULT 6
US-09-006-353A-6
/ Sequence 6, Application US/09006353A
/ Patent No. 6261801
/ GENERAL INFORMATION:
/ APPLICANT: WEI, YING-FEI
/ APPLICANT: YU, GUO-LIANG
/ APPLICANT: GENTZ, REINER
/ APPLICANT: RUBEN, STEVEN
/ TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: HUMAN GENOME SCIENCES, INC.
/ STREET: 9410 KEY WEST AVENUE
/ CITY: ROCKVILLE
/ STATE: MD
/ COUNTRY: US
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/006,353A
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
```

```
/ NAME: BROOKES, ANDERS A
/ REGISTRATION NUMBER: 36,373
/ REFERENCE/DOCKET NUMBER: PF341
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (301) 309-8504
/ TELEFAX: (301) 309-8512
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 415 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-09-006-353A-6

Query Match          68.0%; Score 771; DB 3; Length 415;
Best Local Similarity 70.7%; Pred. No. 7,1e-65;
Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;

QY 1 SGPQAVPPVASENQTCDQEKYEYEPQHRICCSRCPPGTIVSAKCSRIQDTVCATCAENS 60
   |||||
Db 28 SGPQLVPPPIENQTCWDQKEYEYEPMDVCCSRCPGEFVAVCSRSODIVCTCPHNS 87
   |||||

QY 61 YNEHWNVLTICQLCRPCDPVWGLEIAPCTSKRTQCRQCPGMFCAMALECTHC--ELL 118
   |||||
Db 88 YNEHWNHLSCTQLCRPCDVLVGFEEVAPCTSDRAECRCQPGMSCVYLNECVHCEBERL 147
   |||||

QY 119 SDPCPGTEALKDEVGKNNHCVPCKAGHFONTSSPSARCQPHTRCENQGLVEAAPGTAQ 178
   |||||
Db 148 VLCQPGTEAEVTDIMTDVNCVPCCKGHEFNTSSPRARCQPHTRCEIQGLVEAAPGTSY 207
   |||||

QY 179 SDTTCKNPLEP 189
   |||||
Db 208 SDTICKNPPRP 218
   |||||

RESULT 7
US-09-573-986-6
/ Sequence 6, Application US/09573986
/ Patent No. 6455040
/ GENERAL INFORMATION:
/ APPLICANT: Wei, Ying-Fei
/ APPLICANT: Ni, Jien
/ APPLICANT: Gentz, Reiner
/ APPLICANT: Ruben, Steven
/ TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
/ FILE REFERENCE: 1488,1280004
/ CURRENT APPLICATION NUMBER: US/09/573,986
/ CURRENT FILING DATE: 2000-05-18
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: Patent Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 415
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-573-986-6

Query Match          68.0%; Score 771; DB 4; Length 415;
Best Local Similarity 70.7%; Pred. No. 7,1e-65;
Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;

QY 1 SGPQAVPPVASENQTCDQEKYEYEPQHRICCSRCPPGTIVSAKCSRIQDTVCATCAENS 60
   |||||
Db 28 SGPQLVPPPIENQTCWDQKEYEYEPMDVCCSRCPGEFVAVCSRSODIVCTCPHNS 87
   |||||

QY 61 YNEHWNVLTICQLCRPCDPVWGLEIAPCTSKRTQCRQCPGMFCAMALECTHC--ELL 118
   |||||
Db 88 YNEHWNHLSCTQLCRPCDVLVGFEEVAPCTSDRAECRCQPGMSCVYLNECVHCEBERL 147
   |||||

QY 119 SDPCPGTEALKDEVGKNNHCVPCKAGHFONTSSPSARCQPHTRCENQGLVEAAPGTAQ 178
   |||||
Db 148 VLCQPGTEAEVTDIMTDVNCVPCCKGHEFNTSSPRARCQPHTRCEIQGLVEAAPGTSY 207
   |||||
```

```
QY 179 SDTTCKNPLEP 189
   |||||
Db 208 SDTICKNPPRP 218
   |||||

RESULT 8
US-08-866-545-3
/ Sequence 3, Application US/08866545
/ Patent No. 626535
/ GENERAL INFORMATION:
/ APPLICANT: Greene, Mark I.
/ APPLICANT: Muraki, Ramachandran
/ APPLICANT: Takasaki, Wataru
/ TITLE OF INVENTION: PEPTIDES AND PEPTIDE
/ TITLE OF INVENTION: ANALOGUES DESIGNED FROM BINDING SITES OF TUMOR
/ TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR
/ NUMBER OF SEQUENCES: 27
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Pennie & Edmonds LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10036-2811
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/866,545
/ FILING DATE: 30-MAY-1997
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 009113-0004-999
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-493-5556
/ TELEFAX: 650-493-5556
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 77 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: No. 626535e
US-08-866-545-3

Query Match          40.2%; Score 456; DB 3; Length 77;
Best Local Similarity 100.0%; Pred. No. 5,1e-36;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VCATCAENSYNHWNVLTICQLCRPCDPVWGLEIAPCTSKRTQCRQCPGMFCAMALE 111
   |||||
Db 1 VCATCAENSYNHWNVLTICQLCRPCDPVWGLEIAPCTSKRTQCRQCPGMFCAMALE 60
   |||||

QY 112 CTHCELLSDCPGTEAE 128
   |||||
Db 61 CTHCELLSDCPGTEAE 77
   |||||

RESULT 9
US-09-627-775-3
/ Sequence 3, Application US/09627775
/ Patent No. 6682739
/ GENERAL INFORMATION:
/ APPLICANT: Greene, Mark
```


APPLICANT: Murali, Ramachandran
APPLICANT: Aoki, Kazuhiko
APPLICANT: Baron, Roland
TITLE OF INVENTION: Methods of Inhibiting Osteoclastogenesis
FILE REFERENCE: UPN3832
CURRENT APPLICATION NUMBER: US/09/627,775
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/146,090
PRIOR FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 77
TYPE: PRT
ORGANISM: Homo sapiens
US-09-627-775-3

Query Match 40.2%; Score 456; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 5,1e-36;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VCATCAENSYNEHNYLTICQLCPDPPVNGLEBIAPCTSKRTQCRQGMFCAMALE 111
DB 1 VCATCAENSYNEHNYLTICQLCPDPPVNGLEBIAPCTSKRTQCRQGMFCAMALE 60
QY 112 CTHCELLSDCPCPTGEAE 128
DB 61 CTHCELLSDCPCPTGEAE 77

RESULT 10
US-08-974-022-48
Sequence 48, Application US/08974022
Patent No. 6015938
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehaviiland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-Dec-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-022-48

Query Match 26.9%; Score 305; DB 3; Length 227;

Best Local Similarity 35.0%; Pred. No. 2.8e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;
QY 5 AVPPYASE-NQTCRDOEKEYEYPQHRICSCRCPPGTIVSAKCSRIRDTVCATCAENSYNE 63
DB 28 AVPPYAPPEPSTCR--LREYDQTAQWCCSKCSPQAHKVPCTKTSDFVCSCEBSTDYTG 85
QY 64 HNNVLTICQLCR--PCDPVNGLEBIAPCTSKRTQCRQGMFCAMALE-CTHCELLS 119
DB 86 LNNVPECTSCGSCSSDQV---ETQACIREQRICTCRPGWYCALSKQEGCRLCAPLR 141
QY 120 DCPPEG-----TEAPLDEVKGNHVCYPCAGHPONTSPSPARCQHTRCENQGLVDAAP 174
DB 142 KCRPFGVAPRGTSIDV-----CKPCAPGTFTSNTSSTDICRPHQICN---VVAIP 191
QY 175 GTAQSDTTC--KNPLEPLPP 192
DB 192 GNASRDVCTSTSPTRSMAP 211

RESULT 11
US-08-795-445A-48
Sequence 48, Application US/08795445A
Patent No. 6284485
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehaviiland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-445A-48

Query Match 26.9%; Score 305; DB 3; Length 227;
Best Local Similarity 35.0%; Pred. No. 2.8e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

QY 5 AVPPYASE-NQTCRDOEKEYEYPQHRICSCRCPPGTIVSAKCSRIRDTVCATCAENSYNE 63
DB 28 AVPPYAPPEPSTCR--LREYDQTAQWCCSKCSPQAHKVPCTKTSDFVCSCEBSTDYTG 85
QY 64 HNNVLTICQLCR--PCDPVNGLEBIAPCTSKRTQCRQGMFCAMALE-CTHCELLS 119
DB 86 LNNVPECTSCGSCSSDQV---ETQACIREQRICTCRPGWYCALSKQEGCRLCAPLR 141

QY 120 DCPG-----TEAEIKDEYKGNHNHCVCCKXGHPONTSSPASCOPHTRCENOGLVEAAP 174

Db 142 KCRFGGVARPGETSDV-----CKRCAGTFSNTTSSDIDCRPHQICN-----VVAIP 191

QY 175 GTRQSDPTC--KNPELELP 192

Db 192 GNASRDVACTSTSETRSMAP 211

RESULT 12
US-08-795

```

US-08-795-447A-48
Sequence 447, Application US/08795447A
Patent No. 6284728
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David B.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: One Amgen Center Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91362-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,447A
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378D2
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-447A-48

```

Query Match	26.9%;	Score 305;	DB 3;	Length 227;
Best Local Similarity	35.0%;	Pred. No. 2.8e-21;		
Matches 70;	Conservative 24;	Mismatches 78;	Indels 28;	Gaps 9;

QY 5 AVPEFPASE-NQCRQDEKEXEYEPCHRICCSRCPEGVYSAKSRIRDPYCATCAKSNYE 63
 Db 28 APTFAPEEGSGTCR-LREYYDQTAOMCCSKSPGDAKAVFTKTSIDYDCSEBSTYQ 85
 QY 64 HNNYTLICQLCR---PCDFVMGLEIAPCTSKRKTQCRQCPGMFCAMALE-CTHCELLS 119
 Db 86 LMNWVPECLSCGSRSSDPV-----EQATBTRQNRICTRCPGMYCALSKQEGRLCAPR 141
 QY 120 DCPGCG---TEALKDEYKGKNNHCVPCAKGHFQMTSSPSARCQPHTECENQGLVEAP 174
 Db 142 KRPFGGVARPGETESDDV-----CKPACPGTFNSMTSTSDICRPHQICN---VVALP 191
 QY 175 GTAQSDPTTC-KNPLEPLRP 192
 Db 192 GNASRDVACTSTSETRSMAP 211

RESULT 13
US-08-974-186-48
; Sequence 48, Application US/08974186

Patent No. 6284740
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Alczome, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTROPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Denavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,186
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-186-48

Query Match	26.9%;	Score 305;	DB 3;	Length 227;
Best Local Similarity	35.0%;	Pred. No. 2.8e-21;		
Matches	70;	Conservative	24;	Mismatches 78;
				Indels 28;
				Gaps 9;

```

QY      5 AVPPYAS--NOTCRQDEHEVEYEPQHRICCSRPCEPTVYSAKSRIREDYCATCAEVSYN 63
Db      28 AFTPAPEPFGSTCR--LREYYDQTAOMCCSKCPQGHAKVFCITKSDIVCSEDSITYQ 85

QY      64 HNNYITICQLCR---PCDPVMGLEIEIACPTSRKQOCRCOPMFCAMALE--CTHELLS 119
Db      86 LNNVYPECLSCGSRSSDQV---ETQACTRRQNNICTCRPEMVCALSRQEGGRLCAPLR 141

QY      120 DCPPG-----TEAEIKDEYGGKNNHCVPPKAGHFQNTSSPSARCCQHTHCENGLVEAP 174
Db      142 KCRPEFGVARDPELFSDDV-----CKPCAPGFSMTSTSDICRHQICN-----VVALP 192

QY      175 GTAQSDTTC--KNPLELPP 192
Db      192 GNASRDVAVCTSTSPTRMAP 211

```

RESULT 14
 US-08-795-446B-48
 ; Sequence 48, Application US/08795446B
 ; Patent No. 6288032
 ; GENERAL INFORMATION:
 ; APPLICANT: Boyle, William J.
 ; APPLICANT: Lacey, David L.
 ; APPLICANT: Calzone, Frank J.
 ; APPLICANT: Chang, Ming-Shi
 ; TITLE OF INVENTION: OSTEOPROTEGERIN
 ; NUMBER OF SEQUENCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Amgen Inc.

STREET: 1840 Dehaviiland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,446B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wintner, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-446B-48

Query Match 26.9%; Score 305; DB 3; Length 227;
Best Local Similarity 35.0%; Pred. No. 2.8e-21;

Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

QY 5 AVPPYASE-NQTRDQKEYEYEPQHRICGRCPGTYVSACKSRIRDTVCATCAENSYNE 63
DB 28 AFPPYAPEPSTCR--LREYYDQTAQWCCSKCPGQAKVFCYKTSYDVCDSCEDSTYTQ 85
QY 64 HMYVLTICQLCR---PCDPYMGLEIAPCTSKRTQCRQCPMGFCAAMALE-CTHCELLS 119
DB 86 LMMWVECLSCGSRCSDDV---ETQACTREONRICTCRPGWCALSKQEGCRLCAPLR 141
QY 120 DCEPG-----TEALKDEVGKNNHCVPCKAGHFONTSSPARCOPHTRCENGGLVEAAP 174
DB 142 KCRPGGVARPGTETSDV-----CKPCAPGTFSNTSTSDICRPHQICN---VVAIP 191
QY 175 GTAQSDTTC--KNPLEPLPP 192
DB 192 GNASRDVACTSTSPTRSMAP 211

RESULT 15

US-08-706-945D-134
Sequence 134, Application US/08706945D
Patent No. 6369027
GENERAL INFORMATION:
APPLICANT: Boyle, William
APPLICANT: Lacey, David
APPLICANT: Calzone, Frank
TITLE OF INVENTION: Osteoprotegerin
FILE REFERENCE: A-378CIP
CURRENT APPLICATION NUMBER: US/08/706,945D
CURRENT FILING DATE: 1996-09-03
PRIOR APPLICATION NUMBER: 08/577,788
PRIOR FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 145
SOFTWARE: Patentn version 3.1
SEQ ID NO 134
LENGTH: 227
TYPE: prt
ORGANISM: Homo sapiens
US-08-706-945D-134

Query Match 26.9%; Score 305; DB 4; Length 227;
Best Local Similarity 35.0%; Pred. No. 2.8e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

QY 5 AVPPYASE-NQTRDQKEYEYEPQHRICGRCPGTYVSACKSRIRDTVCATCAENSYNE 63
DB 28 AFPPYAPEPSTCR--LREYYDQTAQWCCSKCPGQAKVFCYKTSYDVCDSCEDSTYTQ 85
QY 64 HMYVLTICQLCR---PCDPYMGLEIAPCTSKRTQCRQCPMGFCAAMALE-CTHCELLS 119
DB 86 LMMWVECLSCGSRCSDDV---ETQACTREONRICTCRPGWCALSKQEGCRLCAPLR 141
QY 120 DCEPG-----TEALKDEVGKNNHCVPCKAGHFONTSSPARCOPHTRCENGGLVEAAP 174
DB 142 KCRPGGVARPGTETSDV-----CKPCAPGTFSNTSTSDICRPHQICN---VVAIP 191
QY 175 GTAQSDTTC--KNPLEPLPP 192
DB 192 GNASRDVACTSTSPTRSMAP 211

Search completed: August 27, 2004, 21:11:47
Job time : 34 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 27, 2004, 21:10:31 ; Search time 124 Seconds

(without alignments)
499.829 Million cell updates/sec

Title: US-09-626-219-1

Perfect score: 1133
Sequence: 1 SQFOAVPPYASENQCRDDE.....QSDTCKNPLEPLPMSGRT 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 1297172

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgnt2_6/prodata/2/pubppaa/US07_PUBCOMB.pep:*
2: /cgnt2_6/prodata/2/pubppaa/PCT_NEW_PUB.pep:*
3: /cgnt2_6/prodata/2/pubppaa/US06_NEW_PUB.pep:*
4: /cgnt2_6/prodata/2/pubppaa/US06_PUBCOMB.pep:*
5: /cgnt2_6/prodata/2/pubppaa/US07_NEW_PUB.pep:*
6: /cgnt2_6/prodata/2/pubppaa/PCTUS_PUBCOMB.pep:*
7: /cgnt2_6/prodata/2/pubppaa/US08_NEW_PUB.pep:*
8: /cgnt2_6/prodata/2/pubppaa/US09_PUBCOMB.pep:*
9: /cgnt2_6/prodata/2/pubppaa/US09A_PUBCOMB.pep:*
10: /cgnt2_6/prodata/2/pubppaa/US09C_PUBCOMB.pep:*
11: /cgnt2_6/prodata/2/pubppaa/US09C_PUBCOMB.pep:*
12: /cgnt2_6/prodata/2/pubppaa/US09A_PUBCOMB.pep:*
13: /cgnt2_6/prodata/2/pubppaa/US10A_PUBCOMB.pep:*
14: /cgnt2_6/prodata/2/pubppaa/US10A_PUBCOMB.pep:*
15: /cgnt2_6/prodata/2/pubppaa/US10C_PUBCOMB.pep:*
16: /cgnt2_6/prodata/2/pubppaa/US10C_PUBCOMB.pep:*
17: /cgnt2_6/prodata/2/pubppaa/US60_NEW_PUB.pep:*
18: /cgnt2_6/prodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1133	100.0	197	13	US-10-003-211-1
2	1133	100.0	435	9	US-09-907-372-19
3	1133	100.0	435	9	US-09-768-779A-6
4	1133	100.0	435	10	US-09-917-372-19
5	1133	100.0	435	12	US-10-087-192-942
6	1133	100.0	435	14	US-10-291-480-6
7	1133	100.0	435	15	US-10-369-300-17
8	1133	100.0	435	15	US-10-262-445-133
9	1133	99.6	399	9	US-09-907-372-1
10	1129	99.6	399	10	US-09-917-372-1
11	987	87.1	170	13	US-10-112-793-14
12	970	85.6	172	15	US-10-375-680-57
13	780	68.8	257	9	US-09-948-018-19
14	771	68.0	402	12	US-10-087-192-939
15	771	68.0	415	9	US-09-826-212-6

16	771	68.0	415	9	US-09-907-372-20	Sequence 20, Appl
17	771	68.0	415	9	US-09-935-727-8	Sequence 8, Appl
18	771	68.0	415	10	US-09-917-372-20	Sequence 20, Appl
19	771	68.0	415	14	US-10-186-643-6	Sequence 6, Appl
20	771	68.0	415	15	US-10-418-242-8	Sequence 8, Appl
21	381.5	33.7	305	15	US-10-264-049-3058	Sequence 3058, Ap
22	311.5	27.5	659	14	US-10-363-427-12	Sequence 12, Appl
23	307	27.1	720	14	US-10-363-427-8	Sequence 8, Appl
24	305	26.9	225	9	US-09-840-795-10	Sequence 10, Appl
25	305	26.9	227	11	US-09-405-032-131	Sequence 131, App
26	305	26.9	235	10	US-09-907-263-4	Sequence 4, Appl
27	305	26.9	235	10	US-09-882-735-16	Sequence 16, Appl
28	305	26.9	235	12	US-10-621-783-4	Sequence 4, Appl
29	305	26.9	235	12	US-10-622-383-4	Sequence 4, Appl
30	305	26.9	235	14	US-10-243-230-2	Sequence 2, Appl
31	305	26.9	235	14	US-10-243-230-8	Sequence 8, Appl
32	305	26.9	225	14	US-10-436-826-75	Sequence 75, Appl
33	305	26.9	257	14	US-10-313-852-10	Sequence 10, Appl
34	305	26.9	257	14	US-10-314-033-10	Sequence 10, Appl
35	305	26.9	439	15	US-10-360-101-226	Sequence 226, App
36	305	26.9	450	9	US-09-768-779A-3	Sequence 3, Appl
37	305	26.9	450	14	US-10-291-480-3	Sequence 3, Appl
38	305	26.9	451	9	US-09-800-909-2	Sequence 2, Appl
39	305	26.9	451	9	US-09-826-212-4	Sequence 4, Appl
40	305	26.9	451	9	US-09-758-124-2	Sequence 2, Appl
41	305	26.9	451	9	US-09-896-096A-17	Sequence 17, Appl
42	305	26.9	461	9	US-09-894-924-17	Sequence 17, Appl
43	305	26.9	461	9	US-09-840-070A-17	Sequence 17, Appl
44	305	26.9	461	9	US-09-800-908-3	Sequence 3, Appl
45	305	26.9	461	9	US-09-935-727-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-10-003-211-1
Sequence 1, Application US/10003211
Publication No. US20020197254A1
GENERAL INFORMATION:
APPLICANT: Biogen, Inc.
TITLE OF INVENTION: Soluble Lymphotoxin Beta Receptor and Anti-Lymphotoxin Receptor and Ligand Antibodies as
TITLE OF INVENTION: Therapeutic Agents for the Treatment of Immunological
TITLE OF INVENTION: Diseases
FILE REFERENCE: A013US
CURRENT APPLICATION NUMBER: US/10/003,211
CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: PCT/US97/19436
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/029,060
PRIOR FILING DATE: 1996-10-25
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 197
TYPE: PRT
ORGANISM: Homo Sapien
US-10-003-211-1

Query Match 100.0%; Score 1133; DB 13; Length 197;
Best Local Similarity 100.0%; Pred. No. 7.6e-89;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQFOAVPPYASENQCRDDEKRYEPQHRICCSRCPGTYVSAKSRINDTVCAENLS 60
DB 1 SQFOAVPPYASENQCRDDEKRYEPQHRICCSRCPGTYVSAKSRINDTVCAENLS 60
QY 61 YNEHMYLITICOLCRPCDVMGHEETAPCTSRKTKCRCOPGFCAMALTECHCELSLD 120
DB 61 YNEHMYLITICOLCRPCDVMGHEETAPCTSRKTKCRCOPGFCAMALTECHCELSLD 120

```
QY 121 CPBGTAEELKDEYVGKNNHCVPCKAGHFONTSSPSARCPHTRCENOGIVEAAPTGAQSD 180
DB 121 CPBGTAEELKDEYVGKNNHCVPCKAGHFONTSSPSARCPHTRCENOGIVEAAPTGAQSD 180
QY 181 TTCKNPLEPLPEPMSGT 197
DB 181 TTCKNPLEPLPEPMSGT 197

RESULT 2
US-09-907-372-19
; Sequence 19, Application US/09907372
; Patent No. US20020068242A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Warren, Bridget A.
; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT
; FILE REFERENCE: PC-0050 US
; CURRENT APPLICATION NUMBER: US/09/907,372
; CURRENT FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020068242A1 g339762
US-09-907-372-19

Query Match 100.0%; Score 1133; DB 9; Length 435;
Best Local Similarity 100.0%; Pred. No. 1,7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENS 60
DB 28 SOPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENS 87
QY 61 YNEHWNVLITICQLCRPCDPVWGLEIAPCTSKRTQCRQPGMFCAMALECTHCELLSD 120
DB 88 YNEHWNVLITICQLCRPCDPVWGLEIAPCTSKRTQCRQPGMFCAMALECTHCELLSD 147
QY 121 CPBGTAEELKDEYVGKNNHCVPCKAGHFONTSSPSARCPHTRCENOGIVEAAPTGAQSD 180
DB 148 CPBGTAEELKDEYVGKNNHCVPCKAGHFONTSSPSARCPHTRCENOGIVEAAPTGAQSD 207
QY 181 TTCKNPLEPLPEPMSGT 197
DB 208 TTCKNPLEPLPEPMSGT 224

RESULT 3
US-09-768-779A-6
; Sequence 6, Application US/09768779A
; Patent No. US20020127637A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: MOORE, PAUL
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR
; RECEPTOR-LIKE PROTEIN 8
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/768,779A
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/086,582
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: KENLEY K. HOOVER
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PP368PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-768-779A-6

Query Match 100.0%; Score 1133; DB 9; Length 435;
Best Local Similarity 100.0%; Pred. No. 1,7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENS 60
DB 28 SOPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENS 87
QY 61 YNEHWNVLITICQLCRPCDPVWGLEIAPCTSKRTQCRQPGMFCAMALECTHCELLSD 120
DB 88 YNEHWNVLITICQLCRPCDPVWGLEIAPCTSKRTQCRQPGMFCAMALECTHCELLSD 147
QY 121 CPBGTAEELKDEYVGKNNHCVPCKAGHFONTSSPSARCPHTRCENOGIVEAAPTGAQSD 180
DB 148 CPBGTAEELKDEYVGKNNHCVPCKAGHFONTSSPSARCPHTRCENOGIVEAAPTGAQSD 207
QY 181 TTCKNPLEPLPEPMSGT 197
DB 208 TTCKNPLEPLPEPMSGT 224

RESULT 4
US-09-917-372-19
; Sequence 19, Application US/09917372
; Publication No. US20030068619A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Warren, Bridget A.
; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT
; FILE REFERENCE: PC-0050 US
; CURRENT APPLICATION NUMBER: US/09/917,372
; CURRENT FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030068619A1 g339762
US-09-917-372-19

Query Match 100.0%; Score 1133; DB 10; Length 435;
Best Local Similarity 100.0%; Pred. No. 1,7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENS 60
```

```

Db      28  SGPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENS 87
QY      61  YNEHNNYLTTCQLCRPCDPVWGLEBIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 120
Db      88  YNEHNNYLTTCQLCRPCDPVWGLEBIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 147
QY      121  CPPTGEALKDVEYKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAARGTASD 180
Db      148  CPPTGEALKDVEYKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAARGTASD 207
QY      181  TTCKNPLEPLPEMSGT 197
Db      208  TTCKNPLEPLPEMSGT 224

RESULT 5
US-10-087-192-942
; Sequence 942, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 942
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-192-942

Query Match      100.0%; Score 1133; DB 12; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  SGPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENS 60
Db      28  SGPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENS 87
QY      61  YNEHNNYLTTCQLCRPCDPVWGLEBIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 120
Db      88  YNEHNNYLTTCQLCRPCDPVWGLEBIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 147
QY      121  CPPTGEALKDVEYKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAARGTASD 180
Db      148  CPPTGEALKDVEYKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAARGTASD 207
QY      181  TTCKNPLEPLPEMSGT 197
Db      208  TTCKNPLEPLPEMSGT 224

RESULT 6
US-10-291-480-6
; Sequence 6, Application US/10291480
; Publication No. US2003010069A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Moore, Paul
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Protein 8
; FILE REFERENCE: PP368C1D1
; CURRENT APPLICATION NUMBER: US/10/291,480
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/766,779
```

```

; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/086,582
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/048,020
; PRIOR FILING DATE: 1997-05-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 435
; TYPE: PRT
; ORGANISM: human
US-10-291-480-6

Query Match      100.0%; Score 1133; DB 14; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  SGPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENS 60
Db      28  SGPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENS 87
QY      61  YNEHNNYLTTCQLCRPCDPVWGLEBIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 120
Db      88  YNEHNNYLTTCQLCRPCDPVWGLEBIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 147
QY      121  CPPTGEALKDVEYKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAARGTASD 180
Db      148  CPPTGEALKDVEYKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAARGTASD 207
QY      181  TTCKNPLEPLPEMSGT 197
Db      208  TTCKNPLEPLPEMSGT 224

RESULT 7
US-10-369-300-17
; Sequence 17, Application US/10369300
; Publication No. US20030215442A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Christopher
; APPLICANT: Hancock, Wayne
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF
; TITLE OF INVENTION: IMMUNE
; FILE REFERENCE: 7853-255
; CURRENT APPLICATION NUMBER: US/10/369,300
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/358,463
; PRIOR FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-300-17

Query Match      100.0%; Score 1133; DB 15; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  SGPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENS 60
Db      28  SGPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENS 87
QY      61  YNEHNNYLTTCQLCRPCDPVWGLEBIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 120
Db      88  YNEHNNYLTTCQLCRPCDPVWGLEBIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 147
QY      121  CPPTGEALKDVEYKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAARGTASD 180
Db      148  CPPTGEALKDVEYKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAARGTASD 207
```


QY 181 TTCKNPLEPLPEMSGT 197
DB 208 TTCKNPLEPLPEMSGT 224

RESULT 8
US-10-262-445-133

; Sequence 133, Application US/10262445
; Publication No. US20040014058A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Burgess, Catherine
; APPLICANT: Carterton, Elina
; APPLICANT: Chant, John
; APPLICANT: Chaudhuri, Amitabha
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Giot, Loic
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Mezes, Peter
; APPLICANT: Millet, Isabelle
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Paturajan, Meera
; APPLICANT: Rieger, Daniel
; APPLICANT: Splytek, Kimberly
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Zernusen, Bryan
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS C
; FILE REFERENCE: 21402-462D
; CURRENT APPLICATION NUMBER: US/10/262,445
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/327,454
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,849
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/329,414
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/330,142
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/341,058
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/343,629
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/349,575
; PRIOR FILING DATE: 2001-10-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: CuroSeqLast version 0.1
; SEQ ID NO 133
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-445-133

Query Match 100.0%; Score 1133; DB 15; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOPQAVPPYASENQTCRDEKEYEPQHRICCSRCPPGTIVYSAKCSRIRDTVCATCAENS 60
DB 28 SOPQAVPPYASENQTCRDEKEYEPQHRICCSRCPPGTIVYSAKCSRIRDTVCATCAENS 87

QY 61 YNEHNNYLTICQLCRPCDPVNGLEIAPCTSKRTQCRQCPGMFCAAMALECTHCELLSD 120
DB 88 YNEHNNYLTICQLCRPCDPVNGLEIAPCTSKRTQCRQCPGMFCAAMALECTHCELLSD 147
QY 121 CPGTEALKDQEVGKGNHCVPCXAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
DB 148 CPGTEALKDQEVGKGNHCVPCXAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207
QY 181 TTCKNPLEPLPEMSGT 197
DB 208 TTCKNPLEPLPEMSGT 224

RESULT 9

US-09-907-372-1
; Sequence 1, Application US/09907372
; Patent No. US20020068242A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Warren, Bridget A.
; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT
; FILE REFERENCE: PC-0050 US
; CURRENT APPLICATION NUMBER: US/09/907,372
; CURRENT FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020068242A1 7497867CD1
US-09-907-372-1

Query Match 99.6%; Score 1129; DB 9; Length 399;
Best Local Similarity 99.5%; Pred. No. 3.5e-88;
Matches 196; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOPQAVPPYASENQTCRDEKEYEPQHRICCSRCPPGTIVYSAKCSRIRDTVCATCAENS 60
DB 28 SOPQAVPPYASENQTCRDEKEYEPQHRICCSRCPPGTIVYSAKCSRIRDTVCATCAENS 87
QY 61 YNEHNNYLTICQLCRPCDPVNGLEIAPCTSKRTQCRQCPGMFCAAMALECTHCELLSD 120
DB 88 YNEHNNYLTICQLCRPCDPVNGLEIAPCTSKRTQCRQCPGMFCAAMALECTHCELLSD 147
QY 121 CPGTEALKDQEVGKGNHCVPCXAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
DB 148 CPGTEALKDQEVGKGNHCVPCXAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207
QY 181 TTCKNPLEPLPEMSGT 197
DB 208 TTCKNPLEPLPEMSGT 224

RESULT 10

US-09-917-372-1
; Sequence 1, Application US/09917372
; Publication No. US20030068619A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Warren, Bridget A.
; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT
; FILE REFERENCE: PC-0050 US
; CURRENT APPLICATION NUMBER: US/09/917,372
; CURRENT FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens

```
FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030068619A1 7497867CD1
US-09-917-372-1
Query Match      99.6%; Score 1129; DB 10; Length 399;
Best Local Similarity 99.5%; Pred. No. 3.5e-86;
Matches 196; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQPQAVPPYASENQTCRDQEXEYEPQHRICSCRPPTYVSACSRIRDTVCATCAENS 60
   |||||
Db 28 SQPQAVPPYASENQTCRDQEXEYEPQHRICSCRPPTYVSACSRIRDTVCATCAENS 87
   |||||
QY 61 YNEHNNYLTITICQLCRPCDPVWGLBEIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 120
   |||||
Db 88 YNEHNNYLTITICQLCRPCDPVWGLBEIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 147
   |||||
QY 121 CPPTGTEALKDQEVGKGNHCVCKAGHFNQNTSSPSARCOPTTRCENQGLVEAAPTASDITTK 180
   |||||
Db 148 CPPTGTEALKDQEVGKGNHCVCKAGHFNQNTSSPSARCOPTTRCENQGLVEAAPTASDITTK 207
   |||||
QY 181 TTCNPLEPLPEPMSGT 197
   |||||
Db 208 TTCNPLEPLPEPMSGS 224
   |||||

RESULT 11
US-10-112-793-14
; Sequence 14, Application US/10112793
; Publication No. US20020192729A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,793
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,683A
; FILING DATE: 31-Mar-1997
; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-112-793-14
Query Match      87.1%; Score 987; DB 13; Length 170;
```

```
Best Local Similarity 100.0%; Pred. No. 1.9e-76;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 TCRDQEXEYEPQHRICSCRPPTYVSACSRIRDTVCATCAENSNEHNNYLTITICQLC 74
   |||||
Db 1 TCRDQEXEYEPQHRICSCRPPTYVSACSRIRDTVCATCAENSNEHNNYLTITICQLC 60
   |||||
QY 75 RPCDPVWGLBEIAPCTSKRTQCRQCPGMFCAMALECTHCELLSDCPPTGTEALKDQEVG 134
   |||||
Db 61 RPCDPVWGLBEIAPCTSKRTQCRQCPGMFCAMALECTHCELLSDCPPTGTEALKDQEVG 120
   |||||
QY 135 KGNHCVCKAGHFNQNTSSPSARCOPTTRCENQGLVEAAPTASDITTK 184
   |||||
Db 121 KGNHCVCKAGHFNQNTSSPSARCOPTTRCENQGLVEAAPTASDITTK 170
   |||||

RESULT 12
US-10-375-680-57
; Sequence 57, Application US/10375680
; Publication No. US20040009147A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M
; APPLICANT: Ulrich, Stephen
; APPLICANT: Zhai, Yifan
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
; FILE REFERENCE: 1488,065000E
; CURRENT APPLICATION NUMBER: US/10/375,680
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,234
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)-(17)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-375-680-57
Query Match      85.6%; Score 970; DB 15; Length 172;
Best Local Similarity 98.3%; Pred. No. 5.3e-75;
Matches 169; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
QY 15 TCRDQE--KEYEPQHRICSCRPPTYVSACSRIRDTVCATCAENSNEHNNYLTITICQ 72
   |||||
Db 1 TCRDQEXAAAYEYEPQHRICSCRPPTYVSACSRIRDTVCATCAENSNEHNNYLTITICQ 60
   |||||
QY 73 LCRPCDPVWGLBEIAPCTSKRTQCRQCPGMFCAMALECTHCELLSDCPPTGTEALKDQEV 132
   |||||
Db 61 LCRPCDPVWGLBEIAPCTSKRTQCRQCPGMFCAMALECTHCELLSDCPPTGTEALKDQEV 120
   |||||
QY 133 VGRGNHCVCKAGHFNQNTSSPSARCOPTTRCENQGLVEAAPTASDITTK 184
   |||||
Db 121 VGRGNHCVCKAGHFNQNTSSPSARCOPTTRCENQGLVEAAPTASDITTK 172
   |||||

RESULT 13
US-09-948-018-19
; Sequence 19, Application US/09948018
; Patent No. US2002015097A1
; GENERAL INFORMATION:
; APPLICANT: Theill et al
; TITLE OF INVENTION: TNF RECEPTOR-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCE: 01017/37677
; CURRENT APPLICATION NUMBER: US/09/948,018
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,191
; PRIOR FILING DATE: 2000-09-05
```

NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.1
SEQ ID NO 19
LENGTH: 257
TYPE: PRT
ORGANISM: Mus musculus
US-09-948-018-19

Query Match 68.8%; Score 780; DB 9; Length 257;
Best Local Similarity 100.0%; Pred. No. 1,3e-58;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 EHMNYLTICQLCRPCDPVWGIEIAPCTSKRTQCRCPGMFCAAMALECTHCELLSDCP 122
DB 1 EHMNYLTICQLCRPCDPVWGIEIAPCTSKRTQCRCPGMFCAAMALECTHCELLSDCP 60
QY 123 FGTAEELKDEYVGKGNHCVPCAKGHFQNTSSPSARCPHTRCENQGLVEAAPGTASDTT 182
DB 61 FGTAEELKDEYVGKGNHCVPCAKGHFQNTSSPSARCPHTRCENQGLVEAAPGTASDTT 120
QY 183 CKNPLEPPPEMSGT 197
DB 121 CKNPLEPPPEMSGT 135

RESULT 14

US-10-087-192-939
Sequence 939, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 939
LENGTH: 402
TYPE: PRT
ORGANISM: Mus musculus
US-10-087-192-939

Query Match 68.0%; Score 771; DB 12; Length 402;
Best Local Similarity 70.7%; Pred. No. 1.2e-57;
Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;

QY 1 SQPAVPPYASENQTCRDQKEYEYEPQHRICCSRCPPGTIVYSAKCSRIIDTVYCATCAENS 60
DB 41 SQPAVPPYRIENQTCWQDQKEYEYEPMDVCCSRCPGPFVAVCSRSQDITVCKTCPHNS 100
QY 61 YNEHMNYLTICQLCRPCDPVWGIEIAPCTSKRTQCRCPGMFCAAMALECTHCELLSDCP 118
DB 101 YNEHMNYLTICQLCRPCDPVWGIEIAPCTSKRTQCRCPGMFCAAMALECTHCELLSDCP 160
QY 119 SDCCPTEAEELKDEYVGKGNHCVPCAKGHFQNTSSPSARCPHTRCENQGLVEAAPGTASDTT 178
DB 161 VLQCPGTEAEVTDIMDIDVNCVPCAKGHFQNTSSPSARCPHTRCENQGLVEAAPGTASY 220
QY 179 SDTCKNPPEP 189
DB 221 SDTCKNPPEP 231

RESULT 15
US-09-826-212-6
Sequence 6, Application US/09826212

Patient No. US20010021516A1
GENERAL INFORMATION:
APPLICANT: Wei, Ying-Pei
APPLICANT: Gentz, Reiner
APPLICANT: Ruben, Steven
APPLICANT: Ni, Jian
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
FILE REFERENCE: 1488,1280006
CURRENT APPLICATION NUMBER: US/09/826,212
CURRENT FILING DATE: 2001-04-05
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 415
TYPE: PRT
ORGANISM: Homo sapiens
US-09-826-212-6

Query Match 68.0%; Score 771; DB 9; Length 415;
Best Local Similarity 70.7%; Pred. No. 1.2e-57;
Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;

QY 1 SQPAVPPYASENQTCRDQKEYEYEPQHRICCSRCPPGTIVYSAKCSRIIDTVYCATCAENS 60
DB 28 SQPAVPPYRIENQTCWQDQKEYEYEPMDVCCSRCPGPFVAVCSRSQDITVCKTCPHNS 87
QY 61 YNEHMNYLTICQLCRPCDPVWGIEIAPCTSKRTQCRCPGMFCAAMALECTHCELLSDCP 118
DB 88 YNEHMNYLTICQLCRPCDPVWGIEIAPCTSKRTQCRCPGMFCAAMALECTHCELLSDCP 147
QY 119 SDCCPTEAEELKDEYVGKGNHCVPCAKGHFQNTSSPSARCPHTRCENQGLVEAAPGTASDTT 178
DB 148 VLQCPGTEAEVTDIMDIDVNCVPCAKGHFQNTSSPSARCPHTRCENQGLVEAAPGTASY 207
QY 179 SDTCKNPPEP 189
DB 208 SDTCKNPPEP 218

Search completed: August 27, 2004, 21:22:08
Job time : 127 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 27, 2004, 21:03:31 ; Search time 40 Seconds

(Without alignments)
473.743 Million cell updates/sec

Title: US-09-626-219-1

Sequence: 1 SQQAVPPYASENQTRDQE.....QSDTTCKNPLEPLPEMMSGT 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1133	100.0	435	2	I54182	tumor necrosis fac
2	305	26.9	461	1	A35356	tumor necrosis fac
3	295	26.0	474	2	B38634	tumor necrosis fac
4	290	25.6	459	2	I48854	gene murine tumoun
5	278	24.5	277	2	A60771	B-cell activation
6	243.5	21.5	305	2	A46476	B cell-associated
7	226.5	20.0	651	2	UC7705	death receptor-6 -
8	222.5	19.6	271	2	S12783	OX40 antigen precu
9	214.5	18.9	272	2	I48700	gene oxa4 protein
10	210.5	18.6	455	1	GOHUT1	tumor necrosis fac
11	210	18.5	348	2	T28623	hypothetical protei
12	210	18.5	349	2	D36858	gene G4R protein -
13	207	18.3	349	2	D72175	G2R protein - vari
14	206	18.2	461	2	UC4302	tumor necrosis fac
15	201	17.7	277	2	I37552	OX40 homolog - hum
16	201	17.7	454	1	GOMST1	tumor necrosis fac
17	196	17.3	595	2	A42086	CD30 antigen precu
18	195.5	17.3	255	2	I38426	lymphocyte activat
19	189	16.7	325	2	B43692	t2 protein - rabbi
20	187.5	16.5	314	2	I37383	FAS soluble protei
21	184.5	16.3	461	1	GOPTT1	tumor necrosis fac
22	183.5	16.2	336	1	GOVZML	T2 protein - myxom
23	181	16.0	335	2	A40036	apoptosis-mediatin
24	179.5	15.8	256	2	B32393	T-cell antigen 4-1
25	171.5	15.1	425	1	A26431	nerve growth facto
26	166	14.7	433	2	UC5486	membrane glycoprote
27	164	14.5	416	1	JNCO06	nerve growth facto
28	162	14.3	327	2	A46484	apoptosis-mediatin
29	148.5	13.1	427	1	GOHUN	nerve growth facto

30	145.5	12.8	324	2	UC2395	Fas antigen precur
31	133	11.7	260	1	A46517	CD27 antigen precu
32	132.5	11.7	1111	2	T26972	hypothetical prote
33	129.5	11.4	1620	2	T27283	hypothetical prote
34	129	11.4	3084	1	MMMSA	laminin alpha-1 ch
35	128.5	11.3	1299	2	T43251	furin (EC 3.4.21.7
36	128	11.3	1274	2	T42017	cysteine rich prot
37	126	11.1	3635	2	T10053	laminin alpha 5 ch
38	125.5	11.1	2180	2	T29764	hypothetical prote
39	124.5	11.0	899	2	G02428	subtilisin-like pr
40	124.5	11.0	915	2	JC6148	subtilisin-like pr
41	124.5	11.0	3767	2	S18252	heparan sulfate pr
42	124	10.9	1680	2	A43434	furin (EC 3.4.21.7
43	123.5	10.9	686	2	UC7569	Delta-4 protein -
44	123	10.9	722	2	I48324	DELTA-like 1 - mou
45	122.5	10.8	915	1	A48225	subtilisin-like pr

ALIGNMENTS

RESULT 1
154182
tumor necrosis factor receptor 2-related protein - human
C/Species: Homo sapiens (man)
C/Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C/Accession: I54182
R/Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A/Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen
A/Reference number: I54182; MIM:93252381; PMID:8486360
A/Status: preliminary;
A/Molecule type: mRNA
A/Residues: 1-435 <RES>
A/Cross-references: GB:I04270; NID:9339761; PIRID:AAA36757.1; PID:9339762
C/Genetics:
A/Gene: GDB:LTBR
A/Cross-references: GDB:1230195; OMIM:600979
A/Map position: 12p13.3-12p13.1
C/Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 100.0%; Score 1133; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 2, 3e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	SOQAVPPYASENQTRDQKEYEPOHRIICGRCRPGTYVSAKCSIRIDTVGATCAENS	60
DB	28	SOQAVPPYASENQTRDQKEYEPOHRIICGRCRPGTYVSAKCSIRIDTVGATCAENS	87
QY	61	YNHMYVLTICQICRECPVMGLEIAPCTSKKTKCQCPGMCAMALECTHCELLSD	120
DB	88	YNHMYVLTICQICRECPVMGLEIAPCTSKKTKCQCPGMCAMALECTHCELLSD	147
QY	121	CPGTFABLKDEYKGNHCVPCAKGHFQNTSSPSARCOPHTRCENQGLVEAAPGTAQSD	180
DB	148	CPGTFABLKDEYKGNHCVPCAKGHFQNTSSPSARCOPHTRCENQGLVEAAPGTAQSD	207
QY	181	TTCKNPLEPLPEMMSGT	197
DB	208	TTCKNPLEPLPEMMSGT	224

RESULT 2
A35356
tumor necrosis factor receptor 2 precursor [validated] - human
N/Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C/Species: Homo sapiens (man)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 27-Oct-2003
C/Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R/Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerez, R.; Dower, S.K.
Science 248, 1019-1023, 1990
A/Title: A receptor for tumor necrosis factor defines an unusual family of cellular and

A:Reference number: A35356; MUID:90260639; PMID:2160731
 A:Accession: A35356
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-461 <SMI>
 A:Cross-references: GB:M32315; NID:q189185; PIDN:AAA59929.1; PID:q189186
 R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
 A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occur
 A:Reference number: A36475; MUID:91045991; PMID:2172983
 A:Accession: A36475
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-195, 'R', 197-461 <KOH>
 A:Cross-references: GB:M55944; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
 R:Denbigh, Z.; Loeschner, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M. Cytokine 2, 231-237, 1990
 A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
 A:Reference number: A48416; MUID:91370690; PMID:1966549
 A:Accession: A48416
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 23-461 <DEM>
 A:Cross-references: GB:S63368; NID:g235648; PIDN:AAH19824.1; PID:g235649
 A:Note: sequence extracted from NCBI backbone (NCBI:M63368, NCBI:P63371)
 R:Heiler, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
 A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra
 A:Reference number: A36007; MUID:90349572; PMID:2166946
 A:Accession: A36007
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>
 A:Cross-references: GB:M55857; NID:g339751; PIDN:AAA6362.1; PID:g339752
 R:Loetscher, H.; Schlaeger, E.U.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M. J. Biol. Chem. 265, 20131-20138, 1990
 A:Title: Purification and partial amino acid sequence analysis of two distinct tumor nec
 A:Reference number: A36666; MUID:91056048; PMID:2173696
 A:Accession: A36666
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 23-40; 65-69; 136-141; 300-306 <DOE>
 R:Engelmann, H.; Novick, D.; Wallach, D. J. Biol. Chem. 265, 1531-1536, 1990
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
 A:Reference number: A35010; MUID:90110215; PMID:215136
 A:Accession: A35010
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 27-31 <ENG>
 R:Kuhmert, P.; Kemper, O.; Wallach, D. Gene 150, 381-386, 1994
 A:Title: Cloning, sequencing and partial functional characterization of the 5' region of
 A:Reference number: I38094; MUID:95121934; PMID:7821811
 A:Accession: I38094
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-37 <RES>
 A:Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
 A:Gene: GDB:TNFR2
 A:Cross-references: GDB:125914; OMIM:191191
 A:Map position: 1p36.2-1p36.2
 A:Introns: 26/3
 A:Note: The list of introns is incomplete
 C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo
 C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
 F:40-76/Domain: NGF receptor repeat homology <NG1>
 F:78-119/Domain: NGF receptor repeat homology <NG2>
 F:120-162/Domain: NGF receptor repeat homology <NG3>
 F:164-201/Domain: NGF receptor repeat homology <NG4>

F:262-279/Domain: transmembrane #status predicted <TMN>
 F:280-461/Domain: intracellular #status predicted <INT>
 F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 26.0%; Score 305; DB 1; Length 461;
 Best Local Similarity 35.0%; Pred. No. 6; Le-16;
 Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;
 Oy 5 AVPPYAE NOTGRDQKEVEYEPQHRICGSRCPGTGVSAKCSIRITVCAATCAENSYNE 63
 Db 28 AFTPYAPEPSTCK--LREYIDTAQMKSCSGPQAKVFCITSDVCDSDSTTYQ 85
 Oy 64 HMYVLTICQLCR---PCDPVWGLEIAPCTSKRTQCRCQPGMFCAMALE-CTHCELLS 119
 Db 86 LMMVWPECLCGSGRCSDDY---ETQACIRREQRITCTCPGWCAUSKQEGGRLCAPLR 141
 Oy 120 DCPPG---TEALKDEVGKNNHCYPCRAGHFQNTSSPSARCQPHTRCENGLVEAP 174
 Db 142 KCRPGFVARPGTETSIVV-----CKPCAPGTFSTNTSSDIDCRPHQICN---VVAIP 191
 Oy 175 GTASDPTTC--KNLEPLP 192
 Db 192 GNASMDVCTGSTPTSMAP 211
 RESULT 3
 B38634
 tumor necrosis factor receptor type 2 precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 27-Oct-2003
 C:Accession: B38634; A40254; S54816
 R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.J. Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
 A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor r
 A:Reference number: A38634; MUID:91187885; PMID:1849278
 A:Accession: B38634
 A:Molecule type: mRNA
 A:Residues: 1-474 <LEM>
 A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
 R:Goodwin, R.G.; Anderson, D.; Jerry, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk Mol. Cell. Biol. 11, 3020-3026, 1991
 A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for t
 A:Reference number: A40254; MUID:91246168; PMID:1645445
 A:Accession: A40254
 A:Molecule type: mRNA
 A:Residues: 1-474 <GOO>
 A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
 R:Kisilevsky, M.; Felleman, R.; Felmann, M.; Chernajovsky, Y. submitted to the EMBL Data Library, May 1995
 A:Description: Characterization of the promoter region of the murine p75-TNF receptor.
 A:Reference number: S54816
 A:Accession: S54816
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-22 <KIS>
 A:Cross-references: EMBL:X81128; NID:g809043; PIDN:CAA60618.1; PID:g809044
 C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo
 C:Keywords: cytokine receptor; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
 F:40-77/Domain: NGF receptor repeat homology <NG1>
 F:79-120/Domain: NGF receptor repeat homology <NG2>
 F:166-203/Domain: NGF receptor repeat homology <NG4>
 Query Match 26.0%; Score 295; DB 2; Length 474;
 Best Local Similarity 34.0%; Pred. No. 3; Se-15;
 Matches 66; Conservative 24; Mismatches 84; Indels 20; Gaps 8;
 Oy 8 PYASE-NOTCDQKEVEYEPQHRICGSRCPGTGVSAKCSIRITVCAATCAENSYNEHN 66
 Db 31 PYKPEPGECQISQ--EYIDRAQMKCCACPGQYKHCNCKNSDVLVACDCEASMTYQVWN 89
 Oy 67 YLTICQLCR---PCDPVWGLEIAPCTSKRTQCRCQPGMFC--AMALCTHCELLSDC 121

Db 90 QPRTCLSSSSCTTDYV---ETIRACTKQONRVACACEGARYCALKTHSGSCRCQMRLSKC 145
 QY 122 PPGTEAEIKDEVGKNNHCVCKAGHPONTSSPSARCPHTRCENOGIVEAAPGTAOSDT 181
 Db 146 GPGF-GVASSRAPNGVLCRACAPGTFSDTTSSITDVCPRHICSS---ILAIIFGNASTDA 200
 QY 182 TCKNPLEPLPPEMS 195
 Db 201 VC---APESPTLS 210

RESULT 4

148854 gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)

C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 27-Oct-2003
 C/Accession: 148854
 R/Powell, B.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
 Mamm. Genome 5, 726-727, 1994
 A/Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
 A/Reference number: 148854; MUID:95178848; PMID:7873884
 A/Accession: 148854
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-459 <RES>
 A/Cross-references: EMBL:X/6401; NID:9433830; PIDN:CAA53961.1; PID:9433831
 C/Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homology F/151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 25.6%; Score 290; DB 2; Length 459;
 Best Local Similarity 33.5%; Pred. No. 8, 2e-15;

Matches 65; Conservative 24; Mismatches 85; Indels 20; Gaps 8;

QY 8 PYASE-NQTRDDEKEYEYPQHRICSRCPGTYVSAKCSRIRDTVCATCAENSYNHWN 66
 Db 16 PYRPEPEYEQIQG-EYIDKAKQMCCKCPGQYKHCFCKTSDTVADDEASMTYQWN 74
 QY 67 YLITCOLCR--PCDPYMGLEIAPCTSKKTKCQCPMGFCA-AWALECTHCELLSDC 121
 Db 75 QPRTCLSSSSCTTDYV---ETIRACTKQONRVACACEGARYCALKTHSGSCRCQMRLSKC 130
 QY 122 PPGTEAEIKDEVGKNNHCVCKAGHPONTSSPSARCPHTRCENOGIVEAAPGTAOSDT 181
 Db 131 GPGF-GVASSRAPNGVLCRACAPGTFSDTTSSITDVCPRHICSS---ILAIIFGNASTDA 185
 QY 182 TCKNPLEPLPPEMS 195
 Db 186 VC---APESPTLS 195

RESULT 5

A60771 B-cell activation protein CD40 precursor - human

N/Alternate names: B-cell surface antigen Bp50
 C/Species: Homo sapiens (man)
 C/Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
 C/Accession: S04460; A60771
 R/Stamenkovic, I.; Clark, E.A.; Seed, B.
 EMBO J. 8, 1403-1410, 1989
 A/Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
 A/Reference number: S04460; MUID:89356608; PMID:2475341
 A/Accession: S04460
 A/Molecule type: mRNA
 A/Residues: 1-277 <STA>
 A/Cross-references: EMBL:X/60592; NID:929850; PIDN:CAA43045.1; PID:929851
 R/Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
 J. Immunol. 142, 562-567, 1989
 A/Title: Biochemical characteristics and partial amino acid sequence of the receptor-11X
 A/Reference number: A60771; MUID:89093941; PMID:2463309
 A/Accession: A60771
 A/Molecule type: protein
 A/Residues: 21-50 <BRA>

A/Experimental source: Burkitt lymphoma cell line Raji
 C/Genetics:
 A/Gene: GDB:CD40
 A/Cross-references: GDB:215268; OMIM:109535
 A/Map position: 20q12-20q13.2
 C/Superfamily: CD27 antigen; NGF receptor repeat homology
 C/Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
 F/1-20/Domain: signal sequence #status predicted <SIG>
 F/21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
 F/21-193/Domain: extracellular #status predicted <XTM>
 F/194-215/Domain: transmembrane #status predicted <TM>
 F/216-277/Domain: intracellular #status predicted <CYT>
 F/153/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 24.5%; Score 278; DB 2; Length 277;
 Best Local Similarity 35.0%; Pred. No. 4, 4e-14;

Matches 62; Conservative 20; Mismatches 83; Indels 12; Gaps 5;

QY 7 PYASENQTRDDEKEYEYPQHRICSRCPGTYVSAKCSRIRDTVCATCAENSYNHWN 66
 Db 22 PPTA-----CR-EKQYLI NSQ--CCSLQPGQKLVSDCTEFETETELCPGSEFFDTWN 72
 QY 67 YLITCOLCRCDPVMGLEIAPCTSKKTKCQCPMGFCAWALECTHCELLSDCPGTE 126
 Db 73 RETHQHOKKXCDDPVLGRLVQCKGTSFDTITCTCEBGNHCTSEA--CESCVLHNSCSPFG 130
 QY 127 AEIKDEVGKNNHCVCKAGHPONTSSPSARCPHTRCENOGIVEAAPGTAOSDTTC 183
 Db 131 VK-QIATGVSDTICECPVGFPSNVSAEFKCHWTSCTETDVLVQAGATNKTDVVC 186

RESULT 6

A46476 B cell-associated surface molecule CD40, long splice form - mouse

C/Species: Mus musculus (house mouse)
 C/Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
 C/Accession: A46476; A46515
 R/Torres, R.M.; Clark, E.A.
 J. Immunol. 148, 620-626, 1992
 A/Title: Differential increase of an alternatively polyadenylated mRNA species of murine
 A/Reference number: A46476; MUID:92105763; PMID:1370315
 A/Accession: A46476
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-305 <TOR>
 A/Cross-references: GB:M83112; NID:91553058
 A/Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIPI:75207)
 A/Note: this translation is not annotated in GenBank entry M83CD40A, release 113.0
 R/Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, J.
 J. Immunol. 149, 3921-3926, 1992
 A/Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
 A/Reference number: A46515; MUID:93094586; PMID:1281194
 A/Accession: A46515
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: nucleic acid
 A/Residues: 1-287, 'IV' <GRI>
 A/Cross-references: GB:M83112; NID:91553058; PIDN:AAB08705.1; PID:91553059; GB:M94126; N
 A/Experimental source: BALB/c, liver
 A/Note: sequence extracted from NCBI backbone (NCBIPI:120357)
 C/Comment: For an alternative splice form, see PIR:A46515.
 C/Comment: For an alternative splice form, see PIR:A46476.
 C/Superfamily: CD27 antigen; NGF receptor repeat homology
 C/Keywords: alternative splicing; transmembrane protein
 F/105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 21.5%; Score 243.5; DB 2; Length 305;
 Best Local Similarity 31.0%; Pred. No. 1, 9e-11;

Matches 54; Conservative 22; Mismatches 81; Indels 17; Gaps 5;

QY 15 TCRDDEKEYEYPQHRICSRCPGTYVSAKCSRIRDTVCATCAENSYNHWNLTTCQLC 74
 Db 25 TCSD--KQYLDHGO--CDLCPGSRITSHCTALEKTQCHPCDGSFSAQNNREIRCHOH 80

QY 75 RCPDPVWGLBEIAPCTSKRTQCRQCPGMCAMALECTHCELLSDCPG-----TEAEL 129
 Db 81 RHEPBNGLVKEKGTAEKESDVTCTCKEGQHT--SKCECAQOHTPTCPGGVMEWATET 138
 QY 130 KDEVGKNNHCVPKAGHPONTSSPSARCQPHTRCENOGVLEAAPTASQSDTTTC 183
 Db 139 TDTV-----CHPEPVGFSSNOSLFEKCYFWTSCEDKNLEVLQKGSIQNVIC 186

RESULT 7

JC7705
 death receptor-6 - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 07-Jul-2003
 C:Accession: J07705
 R:Briggs, J.T.; Bode, J.; Goetz, F.W.; Johnson, A.L.
 Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
 A:Title: Conservation of death receptor-6 in avian and piscine vertebrates.
 A:Reference number: J07705; MUID:21308433; PMID:11414698
 A:Accession: J07705
 A:Molecule type: mRNA
 A:Residues: 1-651 <BRI>
 A:Cross-references: GB:AF349908
 C:Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs
 C:Genetics:
 A:Gene: dr-6
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

F.1-21/Domain: signal sequence #status predicted <SIG>
 F.52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
 F.332-350/Domain: transmembrane #status predicted <TM>
 F.410-475/Domain: death domain #status predicted <DD>
 F.551-651/Region: conserved cytoplasmic #status predicted

Query Match 20.0%; Score 226.5; DB 2; Length 651;
 Best Local Similarity 28.8%; Pred. No. 6,5e-10;
 Matches 49; Conservative 26; Mismatches 62; Indels 33; Gaps 6;

QY 30 ICCSRCPGTYVSAKSRIRDTVCATCAENSYNEHMYLTICQLCR-PCDPVWGLBEIAP 88
 Db 50 LICDCPAGTYVSKKCTKSTLRECCSPCDGFTPKHENGIERCHPCRKCE--LPMIEXTH 107
 QY 89 CTSKSKKTQCRCPGMP-----CAAMALECTHCELLSDCP-----PGEAELKDEVKKG 136
 Db 108 CTALTDRECTCLSGTFQJNDTCVPYTV-----CPVGMGVRKKGTETE----- 149
 QY 137 NNHCVPKAGHPONTSSPSARCQPHTRCENOGVLEAAPTASQSDTTCKNP 186
 Db 150 DVCRCPLRGRTSDVPSVYMKCKYTTDCFGKMYVVKGTESDVKCKSP 199

RESULT 8

S12783
 OX40 antigen precursor - rat
 N:Alternate names: nerve growth factor receptor homolog
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
 C:Accession: S12783; S08036
 R:Mallett, S.; Fossum, S.; Barclay, A.N.
 EMBO J. 9, 1063-1068, 1990
 A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocyte
 A:Reference number: S12783; MUID:90214614; PMID:2157591
 A:Accession: S12783
 A:Molecule type: mRNA
 A:Residues: 1-271 <MAL>
 A:Cross-references: EMBL:X17037; NID:957830; PIDN:CAA34897.1; PID:957831
 C:Superfamily: CD27 antigen; NGF receptor repeat homology
 C:Keywords: growth factor receptor; transmembrane protein
 F.1-19/Domain: signal sequence #status predicted <SIG>
 F.20-271/Product: OX40 antigen #status predicted <MA>
 F.111-235/Domain: transmembrane #status predicted <TM>

Query Match 19.6%; Score 222.5; DB 2; Length 271;
 Best Local Similarity 32.1%; Pred. No. 6,7e-10;
 Matches 53; Conservative 17; Mismatches 68; Indels 27; Gaps 5;

QY 21 KEYEPOHRIICSRCPGTYVSAKSRIRDTVCATCAENSYNEHMYLTICQLCRPCDPV 80
 Db 28 KDTYPSGKH-CRCRCQGHGMSRCDHTRDTVCHPCPEPGFYNAVNDT-CKQCTQCNHR 85
 QY 81 MGLEIAPCTSKRTQCRQCPGMCAMALECTHCELLSDCPGEAELKDEVKGNHC 140
 Db 86 SGSELKONCTPTEDTVQCR-----PQTQPR-QDSSHKLGVD 122
 QY 141 VPCKAGHPONTSSPSARCQPHTRCENOGVLEAAPTASQSDTTCKN 185
 Db 123 VPCPGRHFGPSNQA--CKPWTNCTLSGKQIRHPASNSLDVCEHD 165

RESULT 9

148700
 gene ox40 protein - mouse
 N:Alternate names: OX40 antigen
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
 C:Accession: I48700; I48334; S34377
 R:Calderhead, D.M.; Buhmann, J.E.; van den Bertwegh, A.J.; Claassen, E.; Noelle, R.J.; J. Immunol. 151, 5261-5271, 1993
 A:Title: Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell inte
 A:Reference number: I48700; MUID:94044750; PMID:8228223
 A:Accession: I48700
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-722 <RES>
 A:Cross-references: EMBL:Z21674; NID:G312827; PIDN:CAA79772.1; PID:G312828
 R:Bitkeld, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
 Eur. J. Immunol. 25, 926-930, 1995
 A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40 I

A:Reference number: I48334; MUID:95255413; PMID:7737295
 A:Accession: I48334
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-14, 'G', 16-272 <RE2>
 A:Cross-references: EMBL:X85214; NID:G732818; PIDN:CAA59476.1; PID:G732819
 C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 18.9%; Score 214.5; DB 2; Length 272;
 Best Local Similarity 31.7%; Pred. No. 2,7e-09;
 Matches 53; Conservative 16; Mismatches 67; Indels 31; Gaps 6;

QY 21 KEYEPOHRIICSRCPGTYVSAKSRIRDTVCATCAENSYNEHMYLTICQLCRPCDPV 80
 Db 29 KHTYPSGKH-CRCRCQGHGMSRCDHTRDTVCHPCPEPGFYNAVNDT-CKQCTQCNHR 86
 QY 81 MGLEIAPCTSKRTQCRQCPGMCAMALECTHCELLSDCPGEAELKDEVKGNHC 140
 Db 87 SGSELKONCTPTEDTVQCR-----PQTQPR-QDGGYKLGVD 123
 QY 141 VPCKAGHPONTSSPSARCQPHTRCENOGVLEAAPTASQSDTTCKN 185
 Db 124 VPCPGRHFGP-----SPANNACKPWTNCTLSGKQTRHPASNSLDVCEHD 166

RESULT 10

GQHTU1
 tumor necrosis factor receptor 1 precursor [validated] - human
 N:Alternate names: p55 tumor necrosis factor receptor; TNF receptor type 1
 N:Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Dec-2000
 C:Accession: A38208; A34899; A36555; A38281; S12057; J07058; A60231; A38
 R:Fuchs, P.; Strehl, S.; Dvorzak, M.; Himmeler, A.; Ambros, F.F.

Genomics 13, 219-224, 1992
A>Title: Structure of the human TNF receptor 1 (p60) gene (TNFRF1) and localization to chromosome 6
A:Reference number: A38208; MUID:92250049; PMID:1315717
A:Accession: A38208
A:Molecule type: DNA
A:Residues: 1-455 <PUC>
A:Cross-references: GB:M75866; GB:M75865; GB:M75866; NID:g339746; PIDN:AAA61201.1; PID:G339746
R:Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslauer, C.
Cell 61, 351-359, 1990
A>Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor
A:Reference number: A34899; MUID:90235284; PMID:2158862
A:Accession: A34899
A:Molecule type: mRNA
A:Residues: 1-455 <LOC>
A:Cross-references: GB:M58286; GB:M33480; NID:g339753; PIDN:AAA6753.1; PID:g339754
A:Experimental source: placenta
A>Note: part of this sequence, including the amino end of the mature protein, confirmed by Schall, T.J.; Lewis, M.; Koller, K.U.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.
Cell 61, 361-370, 1990
A>Title: Molecular cloning and expression of a receptor for human tumor necrosis factor
A:Reference number: A34900; MUID:90235285; PMID:2158863
A:Accession: A34900
A:Molecule type: mRNA
A:Residues: 1-455 <SCH>
A:Cross-references: GB:M33294; NID:g339744; PIDN:AAA03210.1; PID:g339745
R:Hummel, A.; Maier-Fogay, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantuz, M.; DNA Cell Biol 9, 705-715, 1990
A>Title: Molecular cloning and expression of human and rat tumor necrosis factor receptors
A:Reference number: A36555; MUID:91090841; PMID:1702293
A:Accession: A36555
A:Molecule type: mRNA
A:Residues: 1-455 <HIM>
A:Cross-references: GB:M63121; NID:g339755; PIDN:AAA6754.1; PID:g339756
A:Accession: C36555
A:Molecule type: Protein
A:Residues: 30-38;41-53, 'X','55'-79, 'XX',82-94, 'NK','XX',100-104;107-128;162-167, 'X',169-200, 'X',203-204, 'X',207-208, 'X',211-212, 'X',215-216, 'X',219-220, 'X',223-224, 'X',227-228, 'X',231-232, 'X',235-236, 'X',239-240, 'X',243-244, 'X',247-248, 'X',251-252, 'X',255-256, 'X',259-260, 'X',263-264, 'X',267-268, 'X',271-272, 'X',275-276, 'X',279-280, 'X',283-284, 'X',287-288, 'X',291-292, 'X',295-296, 'X',299-300, 'X',303-304, 'X',307-308, 'X',311-312, 'X',315-316, 'X',319-320, 'X',323-324, 'X',327-328, 'X',331-332, 'X',335-336, 'X',339-340, 'X',343-344, 'X',347-348, 'X',351-352, 'X',355-356, 'X',359-360, 'X',363-364, 'X',367-368, 'X',371-372, 'X',375-376, 'X',379-380, 'X',383-384, 'X',387-388, 'X',391-392, 'X',395-396, 'X',399-400, 'X',403-404, 'X',407-408, 'X',411-412, 'X',415-416, 'X',419-420, 'X',423-424, 'X',427-428, 'X',431-432, 'X',435-436, 'X',439-440, 'X',443-444, 'X',447-448, 'X',451-452, 'X',455-456, 'X',459-460, 'X',463-464, 'X',467-468, 'X',471-472, 'X',475-476, 'X',479-480, 'X',483-484, 'X',487-488, 'X',491-492, 'X',495-496, 'X',499-500, 'X',503-504, 'X',507-508, 'X',511-512, 'X',515-516, 'X',519-520, 'X',523-524, 'X',527-528, 'X',531-532, 'X',535-536, 'X',539-540, 'X',543-544, 'X',547-548, 'X',551-552, 'X',555-556, 'X',559-560, 'X',563-564, 'X',567-568, 'X',571-572, 'X',575-576, 'X',579-580, 'X',583-584, 'X',587-588, 'X',591-592, 'X',595-596, 'X',599-600, 'X',603-604, 'X',607-608, 'X',611-612, 'X',615-616, 'X',619-620, 'X',623-624, 'X',627-628, 'X',631-632, 'X',635-636, 'X',639-640, 'X',643-644, 'X',647-648, 'X',651-652, 'X',655-656, 'X',659-660, 'X',663-664, 'X',667-668, 'X',671-672, 'X',675-676, 'X',679-680, 'X',683-684, 'X',687-688, 'X',691-692, 'X',695-696, 'X',699-700, 'X',703-704, 'X',707-708, 'X',711-712, 'X',715-716, 'X',719-720, 'X',723-724, 'X',727-728, 'X',731-732, 'X',735-736, 'X',739-740, 'X',743-744, 'X',747-748, 'X',751-752, 'X',755-756, 'X',759-760, 'X',763-764, 'X',767-768, 'X',771-772, 'X',775-776, 'X',779-780, 'X',783-784, 'X',787-788, 'X',791-792, 'X',795-796, 'X',799-800, 'X',803-804, 'X',807-808, 'X',811-812, 'X',815-816, 'X',819-820, 'X',823-824, 'X',827-828, 'X',831-832, 'X',835-836, 'X',839-840, 'X',843-844, 'X',847-848, 'X',851-852, 'X',855-856, 'X',859-860, 'X',863-864, 'X',867-868, 'X',871-872, 'X',875-876, 'X',879-880, 'X',883-884, 'X',887-888, 'X',891-892, 'X',895-896, 'X',899-900, 'X',903-904, 'X',907-908, 'X',911-912, 'X',915-916, 'X',919-920, 'X',923-924, 'X',927-928, 'X',931-932, 'X',935-936, 'X',939-940, 'X',943-944, 'X',947-948, 'X',951-952, 'X',955-956, 'X',959-960, 'X',963-964, 'X',967-968, 'X',971-972, 'X',975-976, 'X',979-980, 'X',983-984, 'X',987-988, 'X',991-992, 'X',995-996, 'X',999-1000, 'X',1003-1004, 'X',1007-1008, 'X',1011-1012, 'X',1015-1016, 'X',1019-1020, 'X',1023-1024, 'X',1027-1028, 'X',1031-1032, 'X',1035-1036, 'X',1039-1040, 'X',1043-1044, 'X',1047-1048, 'X',1051-1052, 'X',1055-1056, 'X',1059-1060, 'X',1063-1064, 'X',1067-1068, 'X',1071-1072, 'X',1075-1076, 'X',1079-1080, 'X',1083-1084, 'X',1087-1088, 'X',1091-1092, 'X',1095-1096, 'X',1099-1100, 'X',1103-1104, 'X',1107-1108, 'X',1111-1112, 'X',1115-1116, 'X',1119-1120, 'X',1123-1124, 'X',1127-1128, 'X',1131-1132, 'X',1135-1136, 'X',1139-1140, 'X',1143-1144, 'X',1147-1148, 'X',1151-1152, 'X',1155-1156, 'X',1159-1160, 'X',1163-1164, 'X',1167-1168, 'X',1171-1172, 'X',1175-1176, 'X',1179-1180, 'X',1183-1184, 'X',1187-1188, 'X',1191-1192, 'X',1195-1196, 'X',1199-1200, 'X',1203-1204, 'X',1207-1208, 'X',1211-1212, 'X',1215-1216, 'X',1219-1220, 'X',1223-1224, 'X',1227-1228, 'X',1231-1232, 'X',1235-1236, 'X',1239-1240, 'X',1243-1244, 'X',1247-1248, 'X',1251-1252, 'X',1255-1256, 'X',1259-1260, 'X',1263-1264, 'X',1267-1268, 'X',1271-1272, 'X',1275-1276, 'X',1279-1280, 'X',1283-1284, 'X',1287-1288, 'X',1291-1292, 'X',1295-

QY	18	DOEK-----EYEPDHR-ICCSRCPGTYVSAKC-SRIIDTVCAATCAENSYNEHWNY	67
DB	36	DEKRDVCPDGKGYKIPDNNISICTCKHKGTYIYNDCPGPDQDTPDCRCESGSPASENH	95
QY	68	LTICQLCRCPDPMGLGEETIAPCTSKRKTQCRQCPGMCAMAA---LQETHIELSDCPFG	124
DB	96	LRHCISGSCSKCRKEMGVEIISCTVYKRDITVCGCRNQYRHHWSENLFOCFNESSL--CLNG	152
QY	125	TEAEIKDEVGKANNHCVPCKAGHF--QNTSSPARCOPHTRECENQGL--VAAGGTAOSD	180
DB	153	TVHLSCOE--KONTVCT-CHAGFFLRNECVCSGNCKKSLCCTKTLCTPQIENWVGSTEDSG	209
QY	181	TTCKNPL 187	
DB	210	TTVLLPL 216	

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 27, 2004, 20:54:45 ; Search time 128 Seconds

(without alignments)
434.858 Million cell updates/sec

Title: US-09-626-219-1

1133

Perfect score: 1 SQPAPVPPYSENQTCRDE.....QSDTCKNPDEPPENSGT 197

Sequence:

Scoring table: BLOSUM62

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1133	100.0	197	2	AAW23220 Extracellular
2	1133	100.0	197	2	AAW23220 Extracellular
3	1133	100.0	435	6	ABP96137 Human lym
4	1133	100.0	435	6	ABP96137 Human lym
5	1133	100.0	435	6	ABR40220 Human gen
6	1129	99.6	399	6	ABU89821 TNP-recep
7	1108	97.8	416	7	ADCA2856 Human TNF
8	987	87.1	170	6	ADA49700 Extracell
9	771	68.0	415	6	ABP96138 Human lym
10	771	68.0	415	6	ABP96138 Human lym
11	456	40.2	77	4	AAW94642 TNF-R ext
12	456	40.2	77	4	AAW94642 TNF-R ext
13	381.5	33.7	305	5	ABP41936 Human TNF
14	315	27.8	518	2	AAW23270 Tumour ne
15	311.5	27.5	659	6	ABU57103 Concatame
16	309	27.3	720	6	ABJ37101 Concatame
17	307	27.1	720	6	ABJ37101 Concatame
18	305	26.9	225	6	AAW77463 Primate p
19	305	26.9	225	6	AAW77463 Primate p
20	305	26.9	227	4	AAW69681 Human tum
21	305	26.9	235	2	AAW52965 Human sol
22	305	26.9	235	2	AAW52965 Human sol
23	305	26.9	235	3	AAW69234 Tumour ne
24	305	26.9	235	3	AAW69234 Tumour ne
25	305	26.9	235	3	AAW54440 Amino aci
					AAW54443 Wild type

26	305	26.9	235	4	AAW37685
27	305	26.9	235	6	ADA20593
28	305	26.9	248	3	AAW94718
29	305	26.9	355	6	ADA09891
30	305	26.9	461	2	AAW11141
31	305	26.9	461	2	AAW11001
32	305	26.9	461	2	AAW42058
33	305	26.9	461	3	AAW01342
34	305	26.9	461	3	AAW18717
35	305	26.9	461	3	AAW37801
36	305	26.9	461	4	AAW35331
37	305	26.9	461	4	AAW37686
38	305	26.9	461	4	AAW36698
39	305	26.9	461	5	AAW75172
40	305	26.9	461	5	AAW75174
41	305	26.9	461	5	AAW75173
42	305	26.9	461	5	AAW52451
43	305	26.9	461	6	ABW55854
44	305	26.9	461	6	ABW39799
45	305	26.9	461	6	ABW53256

ALIGNMENTS

RESULT 1
AAW23220
ID AAW23220 standard; protein; 197 AA.

AAW23220;

29-OCT-1997 (first entry)

Extracellular domain of human lymphotoxin beta receptor.

Human, lymphotoxin beta; receptor; blocking agent; extracellular;
ligand binding; domain; treatment; Th1 cell; immune response; delayed;
hypersensitivity; contact; tuberculosis; granulomatous; graft versus host;
disease; organ rejection; autoimmune; disorder; multiple sclerosis;
insulin dependent diabetes; uveitis; cytokine; sympathetic ophthalmia;
psoriasis; diabetes; Toxoplasma; infection; Mycobacterium; abnormal;
lymphoid organ; development.

OS Homo sapiens.

PN W09703687-A1.

PD 06-FEB-1997.

PF 19-JUL-1996; 96WO-US012010.

PR 21-JUL-1995; 95US-00505606.

PA (BIOT) BIOGEN INC.

PI Browning JL, Benjamin CD, Hochman PS;

WPI; 1997-132373/12.

Compositions comprising lymphotoxin-beta receptor blocking agent - used
to treat autoimmune diseases, e.g. sclerosis, insulin-dependent
diabetes, etc.

Example 1; Page 55-56; 76pp; English.

The present sequence, a human lymphotoxin beta receptor (LT-beta-R)
blocking agent, comprises the extracellular ligand binding domain of the
human LT-beta-R up to the transmembrane region. It can be used to treat a
Th1 cell mediated immune response which contributes to a delayed type
hypersensitivity reaction, preferably contact, tuberculosis type or
granulomatous hypersensitivity, graft versus host disease, organ
rejection or an autoimmune disorder, i.e. multiple sclerosis, insulin
dependent diabetes, sympathetic ophthalmia, uveitis and psoriasis. It can

CC also be used to treat conditions exacerbated by the activities of Th-1
CC type cytokines, or listeria, Toxoplasma or Mycobacterium infection. Its
CC ability to selectively or partially block the LT-beta-R pathway may be
CC useful in the treatment of abnormal lymphoid organ development associated
CC with misexpression or overexpression of signalling by the LT-beta-R
CC pathway. The present LT-beta-R blocking agent is capable of selectively
CC inhibiting Th1, but not Th2 cell dependent immune effector mechanisms. As
CC Th1 cytokines can inhibit Th2 cell dependent responses, the present LT-
CC beta-R blocking agent may also indirectly stimulate certain Th2 cell
CC dependent responses which are normally inhibited by Th1 induced
CC cytokines. Doses of about 1 mg/kg of the present soluble LT-beta-R are
CC expected to be suitable starting doses for optimising treatment

XX Sequence 197 AA;

Query Match 100.0%; Score 1133; DB 2; Length 197;

Best Local Similarity 100.0%; Pred. No. 1e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPPVASENQTCDQDEKEYEPEPHRICCSRCPRGTYSACSRIRDTVCATCENS 60
DB 1 SQPQAVPPVASENQTCDQDEKEYEPEPHRICCSRCPRGTYSACSRIRDTVCATCENS 60

QY 61 YNEHMYLITICQLCRPCDPVWGLBEIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 120
DB 61 YNEHMYLITICQLCRPCDPVWGLBEIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 120

QY 121 CPPTGEALDKDEVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENOGIVEAPGTASD 180
DB 121 CPPTGEALDKDEVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENOGIVEAPGTASD 180

QY 121 CPPTGEALDKDEVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENOGIVEAPGTASD 180
DB 121 CPPTGEALDKDEVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENOGIVEAPGTASD 180

QY 181 TTCNPLEPLPEMSGT 197
DB 181 TTCNPLEPLPEMSGT 197

RESULT 2

AAV31326

ID AAV31326 standard; peptide; 197 AA.

XX AAV31326;

DT 04-OCT-1999 (first entry)

DE Human lymphotoxin (LT)-beta-receptor extracellular region.

XX Lymphotoxin-beta; LT-beta; LT-beta receptor; follicular dendritic cell;
XX immune system; tumour; follicular lymphoma; extracellular domain; human.

XX Homo sapiens.

XX WO938525-A1.

XX 05-AUG-1999.

XX 29-JAN-1999; 99WO-US001928.

XX 30-JAN-1998; 98US-0073112P.

XX 02-FEB-1998; 98US-0073410P.

XX (BIOJ) BIOGEN INC.

XX BROWNING J, Thorbecke J, Tsiasbe V;

XX WPI; 1999-469242/39.

XX New method of treating follicular lymphomas by inhibiting interaction
XX between lymphotoxin-beta and its receptor.

XX Example 1; Page 25-26; 31pp; English.

XX The invention provides a method for arresting or reducing, severity of
XX effects of a tumour by administration of a composition which inhibits the

CC interaction between lymphotoxin (LT)-beta and its receptor. An inhibitor
CC of the interaction between LT-beta and its receptor can be administered
CC for altering the survival or maintenance of follicular dendritic cells in
CC a subject and for altering the architecture of the organs of the immune
CC system. The method is useful for treating tumours, specifically
CC follicular lymphomas. It offers an alternative therapy for those with
CC tumours resistant to traditional chemotherapy. The present sequence
CC represents the extracellular region of the human LTbeta-receptor and
CC comprises the ligand binding domain

XX Sequence 197 AA;

Query Match 100.0%; Score 1133; DB 2; Length 197;

Best Local Similarity 100.0%; Pred. No. 1e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPPVASENQTCDQDEKEYEPEPHRICCSRCPRGTYSACSRIRDTVCATCENS 60
DB 1 SQPQAVPPVASENQTCDQDEKEYEPEPHRICCSRCPRGTYSACSRIRDTVCATCENS 60

QY 61 YNEHMYLITICQLCRPCDPVWGLBEIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 120
DB 61 YNEHMYLITICQLCRPCDPVWGLBEIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 120

QY 121 CPPTGEALDKDEVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENOGIVEAPGTASD 180
DB 121 CPPTGEALDKDEVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENOGIVEAPGTASD 180

QY 121 CPPTGEALDKDEVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENOGIVEAPGTASD 180
DB 121 CPPTGEALDKDEVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENOGIVEAPGTASD 180

QY 181 TTCNPLEPLPEMSGT 197
DB 181 TTCNPLEPLPEMSGT 197

RESULT 3

ABP96137

ID ABP96137 standard; protein; 435 AA.

XX ABP96137;

DT 09-MAY-2003 (first entry)

DE Human TNF receptor 2 related protein/LTRbeta SHQ ID NO:19.

XX Human; tumour necrosis factor receptor 2 related protein variant;
XX TNFR2PV; cytostatic; immunosuppressive; antiasthmatic; gene therapy;
XX TNF signalling; cancer; inflammatory disorder; rheumatoid arthritis;
XX asthma; ulcerative colitis.

XX Homo sapiens.

XX WO2003012037-A2.

XX 13-FEB-2003.

XX 24-JUL-2002; 2002WO-US023684.

XX 27-JUL-2001; 2001US-00917372.

XX (INCY-) INCYTE GENOMICS INC.

XX Lal PG, Warren BA;

XX WPI; 2003-256445/25.

XX New cDNA, useful for preparing a composition for treating a disease or
XX condition associated with increased TNF signaling e.g., cancer of the
XX prostate, ovary, gallbladder, breast, brain, liver or colon, or
XX rheumatoid arthritis, asthma.

XX Disclosure; Fig 2A-C; 64pp; English.

XX The present invention describes human tumour necrosis factor receptor 2
XX related protein variant (TNFR2PV). TNFR2PV has cytostatic, antiasthmatic

CC and immunosuppressive activities, and can be used in gene therapy. The
 CC TNFR2PV cDNA or protein sequences can be used for preparing a composition
 CC for treating a disease or condition associated with increased TNF
 CC signalling e.g., cancer of the prostate, ovary, gallbladder, breast,
 CC brain, liver or colon, or inflammatory disorders, such as rheumatoid
 CC arthritis, asthma or ulcerative colitis. The present sequence represents
 CC a human TNFR2 related protein/LTRbeta amino acid sequence, which is given
 CC in comparison with human TNFR2PV in the exemplification of the present
 CC invention
 XX
 SQ Sequence 435 AA:

Query Match 100.0%; Score 1133; DB 6; Length 435;
 Best Local Similarity 100.0%; Pred. No. 2.3e-78;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPYASENQCRDQEKYEYEPQHRICSRCPPTGYVSAKSRIRDTVATCAENS 60
 DB 28 SQPQAVPYASENQCRDQEKYEYEPQHRICSRCPPTGYVSAKSRIRDTVATCAENS 87
 QY 61 YNEHMYVLTICQLCRPCDPVWGLEIAPCTSKRTQCRQPGMFCAMALECTHCELLSD 120
 DB 88 YNEHMYVLTICQLCRPCDPVWGLEIAPCTSKRTQCRQPGMFCAMALECTHCELLSD 147
 QY 121 CPPTGEAEIKDEVGKGNHCVCKAGHFONTSSPSARCPHTRCENQGLVEAARGTQSD 180
 DB 148 CPPTGEAEIKDEVGKGNHCVCKAGHFONTSSPSARCPHTRCENQGLVEAARGTQSD 207
 QY 181 TTCKNPLEPLPPMSGT 197
 DB 208 TTCKNPLEPLPPMSGT 224

RESULT 4
 ID ABR40220 standard; protein; 435 AA.

AC ABR40220;
 XX
 DT 12-UTN-2003 (first entry)
 XX
 DE Human genoxin.
 XX
 KW Human; genoxin; antiarteriosclerotic; antidiabetic; hypotensive;
 KW antilipemic; anorectic; immunomodulator; cytoskeletal; anti-HIV;
 KW antiinflammatory; cardiant; cerebroprotective; gene therapy;
 KW tumour necrosis factor receptor; TNFR; body mass; weight loss; obesity.
 XX
 OS Homo sapiens.
 XX

FH Key Location/Qualifiers
 FT Peptide 1..30
 FT Protein /label= Signal_peptide
 FT Protein /label= Mature_genoxin
 FT Domain 31..227
 FT Domain /label= Extracellular_domain
 FT Domain 228..248
 FT Domain /label= Transmembrane_domain
 FT Domain 249..435
 FT Domain /label= Intracellular_domain

WO2003011322-A1.

13-FEB-2003.

31-JUL-2002; 2002WO-1B003417.

02-AUG-2001; 2001US-0309917P.

(GENSET) GENSET SA.

Lucas J, Dialynas D, Briggs K;

XX WPI; 2003-256417/25.
 DR N-PSDB; AB299578.

PT Screening for an agonist or antagonist of Genoxin activity, useful for
 PT preventing or treating metabolic disorders, comprises contacting Genoxin
 PT polypeptide with a test compound and determining binding.

PS Example 10; Page 33-34; 37pp; English.

CC The invention relates to a novel method for screening for an agonist or
 CC antagonist of Genoxin activity. The agonists/antagonists of the invention
 CC have antiarteriosclerotic, antidiabetic, hypotensive, antilipemic,
 CC anorectic, immunomodulator, cytoskeletal, anti-HIV, antiinflammatory,
 CC cardiant, and cerebroprotective activity. The polypeptides of the
 CC invention may have a use in gene therapy, and act as tumour necrosis
 CC factor receptor (TNFR) agonists. The method is used to screen for an
 CC agonist or antagonist of Genoxin. The method is useful in metabolic
 CC research, particularly, in discovering compounds that modulate Genoxin
 CC activity or that reduce or increase body mass and maintain weight loss,
 CC and in preventing or treating obesity-related diseases or disorders such
 CC as hyperlipidaemia, atherosclerosis, heart disease, stroke, insulin-
 CC resistant diabetes or hypertension, or for preventing or treating
 CC disorders associated with excessive weight loss, such as cachexia, cancer
 CC related weight loss, acquired immunodeficiency syndrome (AIDS)-related
 CC weight loss, chronic inflammatory disease-related weight loss, or
 CC anorexia. The present sequence represents the human genoxin of the
 CC invention
 XX

SQ Sequence 435 AA;

Query Match 100.0%; Score 1133; DB 6; Length 435;
 Best Local Similarity 100.0%; Pred. No. 2.3e-78;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPYASENQCRDQEKYEYEPQHRICSRCPPTGYVSAKSRIRDTVATCAENS 60
 DB 28 SQPQAVPYASENQCRDQEKYEYEPQHRICSRCPPTGYVSAKSRIRDTVATCAENS 87
 QY 61 YNEHMYVLTICQLCRPCDPVWGLEIAPCTSKRTQCRQPGMFCAMALECTHCELLSD 120
 DB 88 YNEHMYVLTICQLCRPCDPVWGLEIAPCTSKRTQCRQPGMFCAMALECTHCELLSD 147
 QY 121 CPPTGEAEIKDEVGKGNHCVCKAGHFONTSSPSARCPHTRCENQGLVEAARGTQSD 180
 DB 148 CPPTGEAEIKDEVGKGNHCVCKAGHFONTSSPSARCPHTRCENQGLVEAARGTQSD 207
 QY 181 TTCKNPLEPLPPMSGT 197
 DB 208 TTCKNPLEPLPPMSGT 224

RESULT 5
 ID AB089821 standard; protein; 435 AA.

AB089821;

10-UTN-2003 (first entry)

TNF-receptor associated factor 5 (TRAF5) interacting protein #1.

Human; cytoskeletal; DAPK3-Agonist; DAPK3-Antagonist; cancer;

TNF-receptor associated factor 5 interacting protein;

tumour necrosis factor associated factor 5 interacting protein;

TRAF5 interacting protein.

Homo sapiens.

WO2003031571-A2.

17-APR-2003.

PF 02-OCT-2002; 2002MO-US031357.
 XX 05-OCT-2001; 2001US-0327454P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 25-JUN-2002; 2002US-0391342P.
 PR 01-OCT-2002; 2002US-00262445.
 XX (CURA-) CURAGEN CORP.
 PA Alsobrook JP, Burgess CE, Catterton E, Chant JS, Chaudhuri A;
 PI Edinger SR, Gerlach VL, Giot L, Gorman L, Guo X, Kehuda R,
 PI Mezes PS, Millet I, Ooi CE, Paturajan M, Rieger DK, Spytek KA;
 PI Taupier RJ, Zehusen BD, Zhong H, Zhong M;
 DR WPI: 2003-381704/36.
 DR N-PSDB; ACA90237.
 XX New DAPK3 polypeptide, useful for preparing a composition for treating or
 PT preventing e.g., cancer.
 PS Example 20F; Page 240; 253pp; English.
 XX The invention describes an isolated polypeptide comprising any of 33 90-
 CC 1273 amino acid sequences (I) given in the specification or its mature
 CC form, a sequence that is at least 95 % identical to (I), or a sequence
 CC comprising one or more conservative substitutions in the amino acid
 CC sequence of (I). The polypeptide is useful for preparing a composition
 CC for treating or preventing e.g. cancer. This is the amino acid sequence
 CC of a tumour necrosis factor (TNF)-receptor associated factor 5 (TRAF5)
 CC interacting protein associated with the identification of novel human
 CC proteins and their functions
 XX Sequence 435 AA;
 SQ
 Query Match 100.0%; Score 1133; DB 6; Length 435;
 Best Local Similarity 100.0%; Pred. No. 2.3e-78;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SOPQAVPYASENQCRODEKEYEYEPQHRICSCRCPPGTYSAKCSRIKDYTCATCAENS 60
 DB 28 SOPQAVPYASENQCRODEKEYEYEPQHRICSCRCPPGTYSAKCSRIKDYTCATCAENS 87
 QY 61 YNEHNNYLTICQLGRCDPVWGLEIAPCTSKRTQCRQCPGMFCAMALBCTHCELLSD 120
 DB 88 YNEHNNYLTICQLGRCDPVWGLEIAPCTSKRTQCRQCPGMFCAMALBCTHCELLSD 147
 QY 121 CPPGTAEALIKQEVGKGNHCVCCKAGHFOHTSSPSARQCPHRCNOGLVEAPGTAOSD 180
 DB 148 CPPGTAEALIKQEVGKGNHCVCCKAGHFOHTSSPSARQCPHRCNOGLVEAPGTAOSD 207
 QY 181 TTCKNPLELPPEMSGT 197
 DB 208 TTCKNPLELPPEMSGT 224
 RESULT 6
 ID ABP96136 standard; protein; 399 AA.
 AC ABP96136;
 XX
 DT 09-MAY-2003 (first entry)
 XX
 DE Human TNF receptor 2 related protein variant SEQ ID No.1.

XX Human; tumour necrosis factor receptor 2 related protein variant;
 KW TNFR2PV; cytosstatic; immunosuppressive; antiasthmatic; gene therapy;
 KW TNF signalling; cancer; inflammatory disorder; rheumatoid arthritis;
 KW asthma; ulcerative colitis.
 XX
 OS Homo sapiens.
 PN W02003012037-A2.
 PD 13-FEB-2003.
 XX 24-JUL-2002; 2002MO-US023684.
 PF 27-JUL-2001; 2001US-00917372.
 XX (INCY-) INCYTE GENOMICS INC.
 PA Lal EG, Warren BA;
 PI WPI: 2003-256445/25.
 DR N-PSDB; ABZ79717.
 XX New CDNA, useful for preparing a composition for treating a disease or
 PT condition associated with increased TNF signaling e.g., cancer of the
 PT prostate, ovary, gallbladder, breast, brain, liver or colon, or
 PT rheumatoid arthritis, asthma.
 XX Claim 20; Fig 1A-F; 64pp; English.
 PS The present sequence represents human tumour necrosis factor receptor 2
 CC related protein variant (TNFR2PV). TNFR2PV has cytosstatic, antiasthmatic
 CC and immunosuppressive activities, and can be used in gene therapy. The
 CC TNFR2PV cDNA or protein sequences can be used for preparing a composition
 CC for treating a disease or condition associated with increased TNF
 CC signalling e.g., cancer of the prostate, ovary, gallbladder, breast,
 CC brain, liver or colon, or inflammatory disorders, such as rheumatoid
 CC arthritis, asthma or ulcerative colitis
 XX Sequence 399 AA;
 SQ
 Query Match 99.6%; Score 1129; DB 6; Length 399;
 Best Local Similarity 99.5%; Pred. No. 4.3e-78;
 Matches 196; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SOPQAVPYASENQCRODEKEYEYEPQHRICSCRCPPGTYSAKCSRIKDYTCATCAENS 60
 DB 28 SOPQAVPYASENQCRODEKEYEYEPQHRICSCRCPPGTYSAKCSRIKDYTCATCAENS 87
 QY 61 YNEHNNYLTICQLGRCDPVWGLEIAPCTSKRTQCRQCPGMFCAMALBCTHCELLSD 120
 DB 88 YNEHNNYLTICQLGRCDPVWGLEIAPCTSKRTQCRQCPGMFCAMALBCTHCELLSD 147
 QY 121 CPPGTAEALIKQEVGKGNHCVCCKAGHFOHTSSPSARQCPHRCNOGLVEAPGTAOSD 180
 DB 148 CPPGTAEALIKQEVGKGNHCVCCKAGHFOHTSSPSARQCPHRCNOGLVEAPGTAOSD 207
 QY 181 TTCKNPLELPPEMSGT 197
 DB 208 TTCKNPLELPPEMSGT 224
 RESULT 7
 ID ADC42856 standard; protein; 416 AA.
 AC ADC42856;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE REMAP protein #16.
 XX
 KW Cytostatic; Antiarteriosclerotic; Anti-HIV; Antiinflammatory;

KW Antiallergic; Antidiabetic; REMAP; pathogenesis.

OS Homo sapiens.

XX WO2003027228-A2.

XX 03-APR-2003.

XX 16-JUL-2002; 2002WO-US022833.

XX 17-JUL-2001; 2001US-0306020P.

XX 27-JUL-2001; 2001US-0308179P.

XX 02-AUG-2001; 2001US-0309702P.

XX 10-AUG-2001; 2001US-0311476P.

XX 10-AUG-2001; 2001US-0311551P.

XX 10-AUG-2001; 2001US-0311718P.

XX 24-AUG-2001; 2001US-0314798P.

XX 31-AUG-2001; 2001US-0316639P.

XX 07-SEP-2001; 2001US-0317996P.

XX (INCY-) INCYTE GENOMICS INC.

XX Lal PG, Honchell CD, Forsythe IU, Walla NK, Tang TY, Borowsky ML;

XX Barroso I, Yue H, Warren BA, Thangavelu K, Gietzen KU, Azimzai Y;

XX Lee BA, Baughn MR, Gorvaid AE, Duggan BM, Tran B, Li JX, Azimzai Y;

XX Richardson TW, Elliott VS, Zebajadian Y, Tran UK, Yao MG,

XX Peterson DP, Luo W, Leht-Mason PM;

XX WPI; 2003-421156/39.

XX New human receptors and membrane-associated proteins (REMAP), useful for

XX diagnosing, treating or preventing disorders associated with aberrant

XX REMAP expression, e.g. cancer, AIDS, atherosclerosis, hypertension or

XX stroke.

XX Claim 1; SEQ ID NO 16; 115pp; English.

XX The present invention relates to an isolated polypeptide. The

XX polypeptides and polynucleotides are useful in diagnosing, treating and

XX preventing disorders associated with aberrant expression of REMAP, such

XX as cell proliferative, autoimmune/inflammatory, renal, neurological,

XX cardiovascular, metabolic, developmental, endocrine, muscle,

XX infections. These are also useful in assessing the effects of exogenous

XX compounds on the expression of nucleic acids and amino acid sequences of

XX REMAP, in facilitating drug discovery process, and in investigating the

XX pathogenesis of diseases or medical conditions. Expression and

XX purification were achieved using bacterial or virus-based expression

XX systems. The present sequence represents an REMAP protein of the

XX invention.

XX Sequence 416 AA;

XX Query Match

XX Best Local Similarity 97.8%; Score 1108; DB 7; Length 416;

XX Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 6 VPPYASNTCTDQDEKEYEYEPQHRICSRCPGTIVYSACKSRIRDTVCATCAENSYNHEM 65

XX 14 VPPYASNTCTDQDEKEYEYEPQHRICSRCPGTIVYSACKSRIRDTVCATCAENSYNHEM 73

XX 66 NYLTTCQLCRPDDPVWGLAEIAPCTSKRTQCRQPGMFCAMALECTHCELLSDCPPEGT 125

XX 74 NYLTTCQLCRPDDPVWGLAEIAPCTSKRTQCRQPGMFCAMALECTHCELLSDCPPEGT 133

XX 126 EAELEDEVGKGNHCVCKAGHFONTSSPSARCOPHTRCENQGLVEAAGTAQSDTTCKN 185

XX 124 EAELEDEVGKGNHCVCKAGHFONTSSPSARCOPHTRCENQGLVEAAGTAQSDTTCKN 193

XX 186 EAELEDEVGKGNHCVCKAGHFONTSSPSARCOPHTRCENQGLVEAAGTAQSDTTCKN 193

XX 194 EAELEDEVGKGNHCVCKAGHFONTSSPSARCOPHTRCENQGLVEAAGTAQSDTTCKN 193

RESULT 8

ADA49700 ID ADA49700 standard; protein; 170 AA.

XX ADA49700;

XX 20-NOV-2003 (first entry)

XX Extracellular region of human TNFRp (hTNFRp) protein.

XX Apo-2 ligand inhibitor; Apo-2Li; Apo-3; apoptosis; affinity;

XX competitive-type receptor; binding assay; cancer cell; human;

XX TNF receptor family; hTNFRp; cytosolic.

XX Homo sapiens.

XX US2002192729-A1.

XX 19-DEC-2002.

XX 28-MAR-2002; 2002US-00112793.

XX 01-APR-1996; 96US-00625328.

XX 23-SEP-1996; 96US-00710802.

XX 31-MAR-1997; 97US-00828683.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ;

XX WPI; 2003-657226/62.

XX Novel isolated biologically active Apo-2 ligand inhibitor polypeptide, or

XX Apo-3 polypeptide which induces or stimulates apoptotic activity, useful

XX in diagnostic assays.

XX disclosure; Fig 2; 53pp; English.

XX The present invention relates to the isolation of a biologically active

XX Apo-2 ligand inhibitor (Apo-2Li) or Apo-3, and the polynucleotide

XX sequences encoding them. Apo-2Li and Apo-3 are involved in apoptosis. The

XX Apo-2Li and Apo-3 polypeptides are useful in diagnostic assays. Apo-2Li

XX is useful for generating antibodies, as standards in assays for Apo-3 or

XX Apo-2Li, in affinity purification techniques, and in competitive-type

XX receptor binding assays when labelled with radiolabelled, enzymes or

XX fluorophores. Agonistic Apo-3 antibodies are useful for stimulating or

XX inducing apoptosis in cancer cells, and thus have therapeutic utility.

XX The present sequence represents the extracellular region of a human TNF

XX receptor family protein. This sequence is compared with the extracellular

XX region of human Apo-2Li.

XX Sequence 170 AA;

XX Query Match

XX Best Local Similarity 87.1%; Score 987; DB 6; Length 170;

XX Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 15 TRDQKEYEYEPQHRICSRCPGTIVYSACKSRIRDTVCATCAENSYNHEMNYLTTCQLC 74

XX 1 TRDQKEYEYEPQHRICSRCPGTIVYSACKSRIRDTVCATCAENSYNHEMNYLTTCQLC 60

XX 75 RPDQVWGLAEIAPCTSKRTQCRQPGMFCAMALECTHCELLSDCPPEGTAELEKDEVG 134

XX 61 RPDQVWGLAEIAPCTSKRTQCRQPGMFCAMALECTHCELLSDCPPEGTAELEKDEVG 120

XX 135 KGNHCVCKAGHFONTSSPSARCOPHTRCENQGLVEAAGTAQSDTTCK 184

XX 121 KGNHCVCKAGHFONTSSPSARCOPHTRCENQGLVEAAGTAQSDTTCK 170

XX RESULT 9

XX AAB36700

XX	AA	AB36700	standard; protein; 415 AA.
XX	AC	AA	
XX	AC	AB36700;	
DT	DT	15-MAR-2001	(first entry)
XX	DE	Human tumour necrosis factor receptor LTBR protein SEQ ID NO:6.	
XX	XX	Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; necrotic; TRAIL receptor without intracellular domain; diagnosis; cytostatic; tumour necrosis factor related apoptosis inducing ligand; vasotropic; immunosuppressive; neuroprotective; antiviral; antiinflammatory; anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian; gene therapy; restenosis; graft versus host disease; tumour; cancer; apoptotic cell death related disease; autoimmune disorder; cardiovascular disorder; viral infection.	
XX	XX	Homo sapiens.	
XX	XX	MO200071150-A1.	
XX	XX	30-NOV-2000.	
XX	XX	18-MAY-2000; 2000MO-US013515.	
XX	XX	20-MAY-1999; 99US-0135164P.	
XX	XX	(HUMA-) HUMAN GENOME SCI INC.	
XX	XX	Wei Y, Ruben SM, Gentz RL, Ni J;	
XX	XX	WPI; 2001-041051/05.	
XX	XX	Nucleic acid encoding a TRID polypeptide, also referred to as tumor necrosis factor receptor 5, useful in the diagnosis, treatment or prevention of cancer, autoimmune disorders and viral infection.	
XX	XX	Disclosure; Fig 2; 285bp; English.	
XX	XX	The present invention describes the human TRID protein (tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without intracellular domain, also referred to as tumor necrosis factor receptor 5 (TNFR-5 or TR5). TRID has cytostatic, immunosuppressive, neurotropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant, antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic activities, and can be used in gene therapy. The TRID polynucleotides are useful for detecting complementary polynucleotides. TRID proteins and polynucleotides are useful in the treatment of tumours, resistance to parasite, bacteria and viruses, restenosis and graft versus host disease. They are also useful for inducing proliferation of T-cells, endothelial cells and certain haematopoietic cells, to regulate antiviral responses and to prevent certain autoimmune diseases after stimulation of TRID by an agonist or TRAIL binding ligand. The antibodies which bind TRID polypeptides are useful for treating and/or preventing diseases associated with increased or decreased apoptotic cell death. The TRID polynucleotides, proteins, antibodies, agonists and antagonists are useful in the diagnosis, treatment or prevention of: (a) cancer; (b) autoimmune disorders; (c) diseases associated with increased apoptosis; (d) cardiovascular disorders; and (e) viral infection. The present sequence represents a tumour necrosis factor receptor used in comparison with TRID in the exemplification of the present invention	
XX	XX	Sequence 415 AA;	
XX	XX	Query Match 68.0%; Score 771; DB 4; Length 415;	
XX	XX	Best Local Similarity 70.7%; Pred. No. 8.4e-51;	
XX	XX	Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1	
XX	XX	1 SOPQAVPPASAEKOTCRDQDEKYEYEPQHICSRCPGPGYVSAAKSRIRDTVCATCAENS 60	
XX	XX	28 SQQLVPPPIRINQOTCMDDKXEYEPMHVHVCSCRCPGPFVFAVFCRSQDTYCKTCPHNS 87	
XX	XX	61 YNEHMYLITTCQRCEDPVMGLAEIAPCTSRKNTQCRQCPGFCAMVLECTHC--ELL 118	

Db	88	YNENHMHLSLTCQICRCPDVLGPEEYAPCTSRKAECCRQPMSCVYLDNECVHGEERL	147
QY	119	SDCEPGTEAEIKDEVKGNHNCVPCKAGHPONTSSPSARCOPIHRCENGLVEAAPGTAQ	178
Db	148	VLCPGTAEAVDEIMDVTNVCVPCKRGHPQNTSSDPARCCOPIHRCETIGLVEAAPGTSY	207
QY	179	SDTTCKNPLEP	189
Db	208	SDTICKNPEP	218
RESULT 10			
ABP96138			
ID	ABP96138	standard; protein; 415 AA.	
XX	AC	ABP96138;	
XX	DT	09-MAY-2003 (first entry)	
XX	DE	Mouse lymphotoxin-beta receptor protein SEQ ID NO:20.	
XX	KW	Human: tumour necrosis factor receptor 2 related protein variant;	
KW	TNFR2PV; cytosolic; immunosuppressive; antiasthmatic; gene therapy;		
KW	TNFR signaling; cancer; inflammatory disorder; rheumatoid arthritis;		
KW	asthma; ulcerative colitis.		
XX	OS	Mus musculus.	
XX	PN	WC2003012037-A2.	
PD	13-FEB-2003.		
XX	PF	24-JUL-2002; 2002WO-US023684.	
XX	PR	27-JUL-2001; 2001US-00917372.	
XX	PA	(INCY-) INCYTE GENOMICS INC.	
XX	PI	Lal PG, Warren BA;	
XX	DR	WPI, 2003-256645/25.	
XX	PT	New cDNA, useful for preparing a composition for treating a disease or	
XX	PT	condition associated with increased TNF signaling e.g., cancer of the	
XX	PT	prostate, ovary, gallbladder, breast, liver or colon, or	
XX	PT	rheumatoid arthritis, asthma.	
XX	PS	Disclosure; Fig 2A-C; 64pp; English.	
XX	CC	The present invention describes human tumour necrosis factor receptor 2	
XX	CC	related protein variant (TNFR2PV). TNFR2PV has cytosolic, antiasthmatic	
XX	CC	and immunosuppressive activities, and can be used in gene therapy. The	
XX	CC	TNFR2PV cDNA or protein sequences can be used for preparing a composition	
XX	CC	for treating a disease or condition associated with increased TNF	
XX	CC	signalling e.g., cancer of the prostate, ovary, gallbladder, breast,	
XX	CC	brain, liver or colon, or inflammatory disorders, such as rheumatoid	
XX	CC	arthritis, asthma or ulcerative colitis. The present sequence represents	
XX	CC	a mouse lymphotoxin-beta receptor amino acid sequence, which is given in	
XX	CC	comparison with human TNFR2PV in the exemplification of the present	
XX	CC	invention	
XX	Sequence	415 AA;	
QY	Query Match	68.0%; Score 771; DB 6; Length 415;	
Db	Best Local Similarity	70.7%; Pred. No. 8.4e-51;	
	Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1,		
QY	1	SGPOAVPYPASNQCIRGQEKYEYEPQHRICCRCPGGTYYSAKSRIKDYCATCAENS	60
Db	28	SGPOLVPPIRINQCWDQDKKEYEPMHEDVCCSRCPGGEFFAVVCSRSQDITVCKTCPHNS	87
QY	61	YNEHMYLITICLCRPGDVMGLEELAPCTSRKXKQCRQPMFCAMMLECTHC--ELT	118

Db 88 YNEHNHLSTGQLCPDQIVLGFBEVAPCTSDRKAECCQPMSCVYLIDNECVHCEERL 147
 QY 119 SDGPGTAEELKDEYKGNHNCVPCAKGHPONTSSPARCQPHTRCENOGIWEAPGTAQ 178
 Db 148 VLGPGTEAEVYDEIMDTDVNCVPCGPHQNTSSPARCQPHTRCENOGIWEAPGTSY 207
 QY 179 SDTCKNPLEP 169
 Db 208 SDTCKNPPPEP 218

RESULT 11

AAW94642
 ID AAW94642 standard; peptide, 77 AA.

XX AAW94642;
 AC
 XX 29-APR-1999 (first entry)
 DT
 XX TNF-R extracellular Cys-rich domain TNF-R-tp.
 DE
 XX Tumour necrosis factor receptor; TNF-R; autoimmune diseases;
 KW inflammation; septic shock; cachexia; graft versus host disease;
 KW skin allergic reaction; immune complex disease; malaria;
 KW transplantation rejection.

OS Homo sapiens.

PN WO9853842-A1.

PD 03-DEC-1998.

PF 29-MAY-1998; 98WO-US010891.

PR 30-MAY-1997; 97US-00866545.

PA (UYPE-) UNIV PENNSYLVANIA.

PI Greene MI, Murali R, Takasaki W;

DR WEI; 1999-080781/07.

PT New compounds designed from a binding loop of a tumour necrosis factor
 PT receptor - are capable of inhibiting the biological activities of tumour
 PT necrosis factor, e.g., in treating inflammation or autoimmune diseases.

PS Disclosure; Fig 1; 78pp; English.

XX The present invention describes peptides and peptide analogues which
 CC correspond in primary sequence to a binding loop of a tumour necrosis
 CC factor receptor (TNF-R) superfamily member. The compounds are especially
 CC designed from a binding loop of TNF-R p55. They are capable of inhibiting
 CC TNF binding to its cellular receptors and may be used to inhibit the
 CC biological activities of TNF. They may be used in treating TNF-associated
 CC conditions such as acute and chronic inflammatory responses, septic
 CC shock, cachexia, autoimmunity, graft-versus-host disease, skin allergic
 CC reactions, immune complex disease, transplantation rejection and malaria.
 CC Administration is, e.g. oral, transdermal, transmucosal, pulmonary,
 CC subcutaneous, intravenous or intramuscular. Parenteral dosage is 0.1-5
 CC mg/kg/day. The present sequence represents an extracellular Cys-rich
 CC domain of TNF-R from the present invention

XX Sequence 77 AA;

Query Match 40.2%; Score 456; DB 2; Length 77;
 Best Local Similarity 100.0%; Pred. No. 1.5e-27;

Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VCATCAENSYNHMYLITICQLCRPCDPVMGLIEIAPCTSKRKTQCRCPGMFCAMALE 111
 Db 1 VCATCAENSYNHMYLITICQLCRPCDPVMGLIEIAPCTSKRKTQCRCPGMFCAMALE 60

QY 112 CTHCELLSDCPGTAE 128
 Db 61 CTHCELLSDCPGTAE 77

RESULT 12

AAB69194
 ID AAB69194 standard; protein, 77 AA.

AC AAB69194;

DT 30-APR-2001 (first entry)

DE Human TNF-R extracellular Cys-rich domain TNF-R-tp SEQ ID NO:3.

XX Tumour necrosis factor receptor; TNF-R; inhibition; osteoclast;
 KW osteoclastogenesis; bone loss; bone resorption; osteoparathic; cytostratic;
 KW antirheumatic; antiarthritic; antiinflammatory; immunomodulatory;
 KW tumour necrosis factor-related activation-induced cytokine; TRANCE;
 KW receptor activator of NF-kappaB ligand; RANK; osteoporosis;
 KW Paget's disease; metastatic bone disease; rheumatoid arthritis;
 KW periodontal disease; modulating dendritic cell maturation;
 KW T cell proliferation; CD40 receptor system.

OS Homo sapiens.

PN WO200108699-A1.

PD 08-FEB-2001.

PF 28-JUL-2000; 2000WO-US020510.

PR 28-JUL-1999; 99US-0146090P.

PA (UYPE-) UNIV PENNSYLVANIA.

PA (AOKI/) AOKI K.

PA (HORN/) HORNE W C.

PA (BARO/) BARON R.

PI Aoki K, Horne WC, Baron R, Greene MI, Murali R;

DR WEI; 2001-182866/18.

PT Use of peptides and peptide analogs which are TRANCE/RANK inhibitors, for
 PT inhibiting osteoclastogenesis and bone resorption.

PS Disclosure; Fig 1; 81pp; English.

XX The present invention describes a method for inhibiting
 CC osteoclastogenesis and bone resorption. Osteoclastogenesis and bone
 CC resorption inhibiting peptide analogues from the present invention have
 CC osteoparathic, cytostratic, antirheumatic, antiarthritic, antiinflammatory
 CC and immunomodulatory activities, and are tumour necrosis factor (TNF)-
 CC related activation-induced cytokine (TRANCE)/ receptor activator of NF-
 CC kappaB ligand (RANK) inhibitors. The method is useful for treating
 CC disease characterised by bone loss such as osteoporosis, Paget's
 CC disease, metastatic bone disease, rheumatoid arthritis or periodontal
 CC disease, and modulating dendritic cell maturation, T cell proliferation,
 CC and/or CD40 receptor systems. The present sequence represents an
 CC extracellular Cys-rich domain of a tumour necrosis factor receptor (TNF-
 CC R) superfamily member, which is used in the exemplification of the
 CC present invention

XX Sequence 77 AA;

Query Match 40.2%; Score 456; DB 4; Length 77;
 Best Local Similarity 100.0%; Pred. No. 1.5e-27;

Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VCATCAENSYNHMYLITICQLCRPCDPVMGLIEIAPCTSKRKTQCRCPGMFCAMALE 111
 Db 1 VCATCAENSYNHMYLITICQLCRPCDPVMGLIEIAPCTSKRKTQCRCPGMFCAMALE 60

QY 112 CTHCELLSDCPGTEAF 128
 Db 61 CTHCELLSDCPGTEAF 77

RESULT 13

ABP41926 ID ABP41926 standard; protein; 305 AA.

XX ABP41926;

DT 22-AUG-2002 (first entry)

XX Human ovarian antigen HSABJ44, SEQ ID NO:3058.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KM ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KM infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KM PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 KM inflammatory condition; immune disorder; blood disorder;
 KM cardiovascular disorder; respiratory disorder; neurological disorder;
 KM gastrointestinal disorder; urinary system disorder; drug screening;
 KM gene therapy; chromosome mapping; forensic analysis;
 KM antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KM antiinflammatory; gynaecological; reproductive; chromosome 12p13.

XX Homo sapiens.

XX WO200200677-A1.

XX 03-JAN-2002.

XX 07-JUN-2001; 2001WO-US018569.

XX 07-JUN-2000; 2000US-0209467P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Birse CE, Rosen CA;

XX MPI; 2002-147878/19.

XX N-PSDB; AB055003.

XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.

XX Claim 11; SEQ ID NO 3058; 2922pp; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovarian and breast cancer, and
 CC disorders. Such conditions include various origin, reproductive system
 CC metastatic tumours of ovarian or breast origin, anovulation,
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the

CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 305 AA;

Query Match 33.7%; Score 381.5; DB 5; Length 305;
 Best Local Similarity 93.4%; Pred. No. 2,9e-21;
 Matches 71; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 123 PGTEA-ELKDEYKGNHCVCKAGHFOHTSSPSARCOPTRENOGLVEAPGTASDT 181

Db 19 PGMPALFLPPEVKGKNNHCPCCKAGHFOHTSSPSARCOPTRENOGLVEAPGTASDT 78

QY 182 TCKNPLELPPEMSGT 197

Db 79 TCKNPLELPPEMSGT 94

RESULT 14

AAR51003 ID AAR51003 standard; protein; 518 AA.

XX AAR51003;

XX 25-MAR-2003 (revised)

XX 07-OCT-1994 (first entry)

XX Sequence of a recombinant human (rhu) tumour necrosis factor receptor

XX TNFR/Fc fusion protein.

XX Tumour necrosis factor receptor; chimeric antibody molecule;

XX immunoglobulin.

XX Synthetic.

XX WO9406476-A1.

XX 31-MAR-1994.

XX 14-SEP-1993; 93WO-US008666.

XX 15-SEP-1992; 92US-00946236.

XX (IMMV) IMMUNEX CORP.

XX Smith CA, Jacobs CA;

XX MPI; 1994-118172/14.

XX N-PSDB; AA045225.

XX Treating TNF mediated inflammatory diseases with TNF antagonist - esp.

XX soluble form of TNF receptor, opt. as fusion protein with human

XX immunoglobulin Fc region, esp. for treating arthritis.

XX Disclosure; Page 32-34; 47pp; English.

XX AA045224 is cDNA from clone 1 of library WI-26 V4 of human fibroblast

XX cell line WI-26 V4. The mature full-length TNFR1 is a glycoprotein

XX having a mol. wt. of about 75-80 kDa. The cloning of the cDNA for TNFR1

XX was described in Smith et al., Science 248:1019,1990. Clone 1 is

XX contained in expression vector pCAV/NOT-TNFR (ATCC 68088). A recombinant

XX chimeric antibody may be produced having TNFR sequences substituted for

XX the variable domains of either or both of the immunoglobulin molecule

XX heavy and light chains and having unmodified constant region domains. A

XX specific example of a TNFR/Fc fusion protein is given in AA045225/RS1003.

XX The rhu TNFR/Fc fusion gene was created by ligating the following

XX fragments into a cloning vector: 1) an 867 bp Asp718-Pvu2 fragment from

XX pCAV/NOT-TNFR (ATCC 68088) contg. the cDNA encoding the truncated TNFR.

XX 2) a 700 bp StyI-SpeI fragment from plasmid pIX1498 coding for 232 AAs of

CC The Pc portion of human IgG1, p1muid, p1XX496 is a yeast expression
CC vector contg. the Pc fragment of human IgG1. 3) An oligo linker to fuse
CC the truncated TNFR with the human IgG1 Pc fragment. This linker was
CC created by PCR using primer AA045226, which encodes the 3' end of the
CC truncated TNF receptor and the 5' end of human IgG1, and primer AA045227
CC which is an antisense sequence encoding bps 257-237 of human IgG1.
CC (Updated on 25-MAR-2003 to correct PN field.)
CX

Query Match	27.8%	Score 315	DB 2	Length 518
Best Local Similarity	35.5%	Pred. No. 5.9e-16		
Matches 71	Conservative	24	Mismatches	28
			Gaps	9

QY 5 AVPPVASE-NOTCRDDEKKEYEQRHICGSCRPPEGTIVSACSRIKRVYCAITCAENSTINE 63
 Db 57 AAFPVAPPEPSTOR-LREIYDQTAOMCCSKSPQAHKVFCTKTSIDVOCSCBEDSTYTQ 114
 QY 64 HNNVLTTCICLR---PCDPEVGMGLEEIAFPTSKRTQGCOPGMFPAAMALE-CHCELLS 119
 Db 115 LMMVVEPEGLSCGSRCSQDY---ETQACTHEQNRICTCRPGWCALSKQGGCLQAPLR 170
 QY 120 DCPPEG-----TEALIKDEVKGNHNVCPQCKAGHFQNTSSPBARCQPHTRCENQGLVEAP 174
 Db 171 KCRPGGVAPRGTEITSYV-----CKRCARGTSFNTTSSIDICRPHQICN---VVAIP 220
 QY 175 GNAQSDTTC--KNPLEPLP 192
 Db 221 GNASMDAVCTSTSPTRSMAP 240

RESULT 15

ABJ37103
ID ABJ37103 standard; protein; 659 AA.
vv

AC ABJ37103;

DT 08-MAY-2003 (first entry)
VV

DE XX	Concatameric immunoadhesion human protein sequence SEQ ID No 12.

KW Antiinflammatory; antibacterial; immunosuppressive; antirheumatic;
KW antiarthritic; immunomodulator; conalbumin protein, soluble domain;
KW dimeric protein; inflammation; septicæmia; cytotoxicity;
KW rheumatoid arthritis; cachexia; inflammation; human.

OS Homo sapiens.

PN WO2003010202-A1.

06-FEB-2003 PD

26-JUL-2002; 2002WO-KR001427

PR 26-JUL-2001; 2001KR-00045028.
XX

PA (MEDE-) MEDEXGEN CO LTD.
XX

PI Chung Y, Han J, Lee H, Choi E, Kim J;
YX

DR WPI; 2003-229639/22.

DR N-PSDB; ABT32046

PT New concatameric protein having two soluble domains, useful for
PT diagnosing and treating disorders associated with the dimeric protein or
PT its glycosylated form, such as inflammation, septicemia, rheumatoid
PT arthritis and cachexia.

PS Claim 27; Page 148-152; 211pp; English.
vvy

The invention relates to a novel concatameric protein comprising two soluble domains, in which an N-terminus of a soluble domain of a biologically active protein is linked to a C-terminus of an identical

CC soluble domain or a different soluble domain of a biologically active
CC protein. The methods and compositions of the present invention are useful
CC for the diagnosis and treatment of disorders associated with dimeric
CC protein or its glycosylated form, such as inflammation, septicemia,
CC cytotoxicity, rheumatoid arthritis, cachexia and other inflammation-
CC related diseases. This sequence represents the human concatameric protein
CC of the invention

Query Match	27.5%	Score 31.5;	DB 6;	Length 659;
Best Local Similarity	36.4%	Pred. No. 1.4e-15;		
Matches 71; Conservative	23;	Mismatches 74;	Indels 27;	Gaps 9

QY 5 AADPEYASE-NORCCPQOEKEYEYEPQHRICSCPEPTIYSACSRIRDTVCATCANBYNE 63
 Db 28 AATPYAPEBGSTCR-LREIYDQTAOMCCSCSPQAHKAVCTKTSDDVCSCSEDSITYQ 85
 QY 64 HNNVYLITCOLCR---PCDPVMGLEIEIACFCTSKRTQGCQCPGMCACMALE-CTHCEILTS 11
 Db 86 LNNWVPECLSCGSRCSQV---ETACTCEQNRICTCRPGWYCALSKQGCGLCAPLR 141
 QY 120 DCDPEG---TEALIKDEVGANNHCVPCKAGHPONTSSPEARQCPHTRCENQGLVEAP 174
 Db 142 KCRPEFGVAPRGETSTDVY-----CKRCAGTSTNTTSSIDICRPHQICN---VVALP 191
 QY 175 GTAQSDITTCNKLPLEP 189
 Db 192 GNASMDANCTSP-EP 205

Search completed: August 27, 2004, 21:07:57
Job time : 135 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 27, 2004, 21:02:27 ; Search time 115 Seconds

(without alignments)
540.496 Million cell updates/sec

Title: US-09-626-219-1

Perfect score: 1133
Sequence: 1 SQPQAVPYASENQTCDPQE.....QSDTCKNPLEPPEPMSGT 197

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_ivirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	309.5	27.3	483	13 Q800K7	Q800K7 paralichthy
2	295.5	26.1	278	6 Q8SQ34	Q8SQ34 sus scrofa
3	291.5	25.7	433	11 Q912M6	Q912M6 rattus norv
4	291.5	25.7	474	11 Q80WY6	Q80WY6 rattus norv
5	290	25.6	459	11 Q62327	Q62327 mus musculi
6	284.5	25.1	274	6 Q7YK15	Q7YK15 mus musculi
7	278	24.5	223	4 Q86TK5	Q86TK5 homo sapien
8	276.5	24.4	482	11 Q88734	Q88734 mus musculi
9	265.5	23.4	277	6 Q8WMQ2	Q8WMQ2 ovis aries
10	258	22.8	275	11 Q80WM9	Q80WM9 mus musculi
11	253	22.3	462	13 Q805B0	Q805B0 gallus galli
12	243.5	21.5	289	11 Q8K2Y6	Q8K2Y6 mus musculi
13	242.5	21.4	283	6 Q9XSZ8	Q9XSZ8 cercopithec
14	240	21.2	186	12 Q7Z735	Q7Z735 cowpox viru
15	238.5	21.1	318	13 Q7Z735	Q7Z735 oncorhynch
16	238	21.0	302	13 Q9PUS0	Q9PUS0 salvelinus

17	233.5	20.6	457	4 Q81VS6	Q81VS6 homo sapien
18	232.5	20.5	467	13 Q80010	Q80010 gallus galli
19	230	20.3	276	13 Q9DDD2	Q9DDD2 gallus galli
20	230	20.3	351	12 Q57117	Q57117 cowpox viru
21	229.5	20.3	285	11 Q90W71	Q90W71 oncorhynch
22	226.5	20.0	167	12 Q80Y13	Q80Y13 vaccinia vi
23	225.5	19.9	186	13 Q7Z2Y5	Q7Z2Y5 gallus galli
24	225.5	19.9	651	13 Q98SM6	Q98SM6 gallus galli
25	225	19.9	186	12 Q9YPR7	Q9YPR7 cowpox viru
26	225	19.9	349	12 Q57099	Q57099 monkeypox v
27	225	19.9	349	12 Q57098	Q57098 monkeypox v
28	225	19.9	349	12 Q57284	Q57284 camelipox vi
29	223	19.7	186	12 Q911R5	Q911R5 vaccinia vi
30	221.5	19.5	285	13 Q90XS6	Q90XS6 oncorhynch
31	221	19.5	349	12 Q57100	Q57100 monkeypox v
32	221	19.5	349	12 Q57097	Q57097 monkeypox v
33	220.5	19.5	169	11 Q9UKB0	Q9UKB0 rattus norv
34	219	19.3	349	12 Q57102	Q57102 monkeypox v
35	219	19.3	349	12 Q57291	Q57291 monkeypox v
36	218.5	19.3	167	12 Q9DJL2	Q9DJL2 cowpox viru
37	218.5	19.3	350	12 Q57116	Q57116 cowpox viru
38	218	19.2	185	12 Q9W7B4	Q9W7B4 vaccinia vi
39	218	19.2	348	12 Q57108	Q57108 monkeypox v
40	218	19.2	348	12 Q57103	Q57103 monkeypox v
41	217.5	19.2	267	6 Q02764	Q02764 oxycetolagus
42	216.5	19.1	167	12 Q72762	Q72762 cowpox viru
43	216	19.1	348	12 Q57277	Q57277 monkeypox v
44	216	19.1	349	12 Q57101	Q57101 monkeypox v
45	210	18.5	348	12 Q57112	Q57112 variola vir

ALIGNMENTS

RESULT 1

Q800K7 PRELIMINARY; PRT; 483 AA.
ID Q800K7
AC Q800K7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tumor necrosis factor receptor-2.
GN TNFR-2.
OS Paralichthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralichthyidae; Paralichthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RA Park C., Kurobe T., Hirano I., Aoki T.;
RT "Cloning and characterization of cDNAs for two distinct tumor necrosis
factor receptor superfamily genes from Japanese Flounder Paralichthys
RT olivaceus."
RU Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB080947; BAC65226.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 3.
DR SMART; SM00208; TNFR_4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00650; TNFR_NGFR_2; 3.
KW Receptor.
SQ
SEQUENCE 483 AA; 52227 MW; EE5874A8C7F2085 CRC64;

Query Match 27.3%; Score 309.5; DB 13; Length 483;
Best Local Similarity 35.4%; Pred. No. 2.9e-25;

Matches 64; Conservative 20; Mismatches 80; Indels 17; Gaps 6;

QY 16 GADQKEYEYEPQHRCCRCRPGTVSAKCSIRITVCATCAENSYNEHMYLTTCQLCR 75
Db 27 CHNSTTEYRED--VCKKCPGQRLIQKCDPATESVCKQCDSDGQYMEKWNVAQKCLSCN 84

QY 76 PCDPVWGLEIAPCTSKRKTCRCOPGMFCMAWLE-----CHCELLSDCPPTAEIK 130
 DB 85 KCSNNGNLOVAGRCSSRTTRGCVCKRPMYC---IMFDNPYCAECNYSQCRAGYVSLP 141
 QY 131 DEVGKGN--HCVPCKAGHONTSSSPARCOPHTRCNOCGLVEAPGTASDTCKNPLE 188
 DB 142 ---GKANSDVKCELCPPGMSNTSSNTETCRPHDCHGKAVR--KNTTSDIVCEBGVA 196
 QY 189 P 189
 DB 197 P 197

RESULT 2

Q8SQ34 PRELIMINARY; PRT; 278 AA.
 AC Q8SQ34; 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE CD40.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID=9823;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA West K.A., Li A.W., Rowden G.;
 RT "Characterization of the Porcine CD40 Molecule."
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF248545; AAL2924.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.
 DR GO; GO:0007165; P:immune response; IEA.
 DR GO; GO:0070165; P:signal transduction; IEA.
 DR InterPro; IPR008063; Fas_receptor.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR PRINTS; PR01680; FASRECEPTOR.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 4.
 DR PROSITE; PS50050; TNFR_NGFR_2; 4.
 SQ SEQUENCE 278 AA; 30951 MW; 20D446E4AF93DD2 CRC64;

Query Match 26.1%; Score 295.5; DB 6; Length 278;
 Best Local Similarity 36.9%; Pred. No. 5.4e-24;
 Matches 62; Conservative 19; Mismatches 74; Indels 13; Gaps 3;

QY 21 KEYEPQHRICSSRCPPGTIVYSAKCSRIDTVCATCAENSYEHNNYLTICQLCRPCDPV 80
 DB 27 KENQVPTNSRCNLCPPGQKLVNHCETEVEETCLPSSSEFLATNMRKHCHQHKYCDPN 86
 QY 81 MGLERIAPCTSKRKTCRCOPGMFCMAWLECHCELLSDCPG-----TEAEIKDEVGK 135
 DB 87 LELQVQREGSTISDTTCTVCSSEGHCHNSA--CESCTLHLCLCPGLGVKQMAHEVSTI-- 142
 QY 136 GNNHCVPCKAGHONTSSSPARCOPHTRCNOCGLVEAPGTASDTTC 183
 DB 143 ----CPCPVGPFNSNVSASEKQPWTSCSKGLVQRAGTNTDVC 186

RESULT 3
 Q91ZM6 PRELIMINARY; PRT; 433 AA.
 AC Q91ZM6;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Tumor necrosis factor receptor type II (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA STRAIN=Sprague-Dawley;
 RA Osburg B., Pelser C., Doemling D., Schomburg L., Voigt K., Bickel U.;
 RT "TNF-receptors p60 and p80 are constitutively expressed by rat brain
 capillary endothelial cells and participate in TNF-alpha transport
 through the blood-brain barrier."
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF420214; AAL16021.1; -.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS50050; TNFR_NGFR_2; 3.
 DR PROSITE; PS50050; TNFR_NGFR_2; 3.
 KM Receptor.
 FT NON TER 1
 FT NON TER 433
 SQ SEQUENCE 433 AA; 45723 MW; 75736D835E72CA4A CRC64;

Query Match 25.7%; Score 291.5; DB 11; Length 433;
 Best Local Similarity 33.3%; Pred. No. 2.3e-23;
 Matches 65; Conservative 24; Mismatches 91; Indels 15; Gaps 7;

QY 8 PYASENQTCRDOKEYEPQHRICSSRCPPGTIVYSAKCSRIDTVCATCAENSYEHNNY 67
 DB 11 PYKEPQNGQOISQEIYDKAQCACPCPQYAKHFNCNKTSDIVCADCAAGMFTQWNH 70
 QY 68 LTTICQLC-RPC--DPVWGLEIAPCTSKRKTCRCOPGMFCA--AMALECHCELLSDCP 122
 DB 71 LHTCLCSSSCSDQV---ETHNCTKQNVCACMADSYALKLHSGNCQCKLSCG 126
 QY 123 PGTAEIKDVGKNNHCVPCKAGHONTSSSPARCOPHTRCNOCGLVEAPGTASDTT 182
 DB 127 PGF-GVARSRTSNANVICSACAPGTFSDTTSIVCRHRICS-----ILAIQNASTDAV 181
 QY 183 CKNPLEPLPPMSGT 197
 DB 182 CASE-SPTPSAVPRT 195

RESULT 4

Q80WY6 PRELIMINARY; PRT; 474 AA.
 AC Q80WY6;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Tumor necrosis factor receptor type II.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA STRAIN=Wistar; TISSUE=Spleen;
 RA Li Y., Ji A., Schafer M.K.;
 RT "Expression of TNFR2 in rat dorsal root ganglion."
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF498039; AAP3151.1; -.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS50050; TNFR_NGFR_2; 3.
 KM Receptor.
 SQ SEQUENCE 474 AA; 50148 MW; 298C6AB9E8C8D714 CRC64;

Query Match 25.7%; Score 291.5; DB 11; Length 474;
 Best Local Similarity 33.3%; Pred. No. 2.6e-23;

Matches 65; Conservative 24; Mismatches 91; Indels 15; Gaps 7;

QY PYASENQTCRDEKEYEYEPQHRICSCRCPPGTVYSAKCSRIPTVCATCAENSYNEHMYL 67
 Db 31 PYKPEPGYEQCISO EYDRAKQMCACACPCGGQYVKKHCNNTSDIVGCADCSAMWTQVWN 74
 QY 68 LTIICQLC-RPC--DPVWGLGEIAPCTSKRTQCRCPGFCA--AMALECTHCELLSDCP 122
 Db 91 LHTICLSSSSCSDDV---ETHNCTKKQNRVCAQMAQSYCAKLHSGNCRQCKLSKCG 146
 QY 123 PGTEALIKDEVKGNHCVCPKAGHFQNTSSPSARCOPTHRCENQGLVEAPGTAQSDTT 182
 Db 147 PGF-GVAASRTSNGNVISACAPGTFSDTTSITVCRPHRIS---TLALPGASTDAV 201
 QY 183 CKNPLEPLPPPMSCGT 197
 Db 202 CASE-SPTPSAVPRT 215

RESULT 5
 Q62327 PRELIMINARY; PRT; 459 AA.
 ID Q62327
 AC Q62327
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Murine tumour necrosis factor receptor 2 protein (Fragment).
 GN TNFRSF1B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD.
 RX MEDLINE=95178848; PubMed=7873884;
 RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
 RT "Allelic variation of the type 2 tumor necrosis factor receptor
 RT linked to autoimmune diabetes in NOD mice.";
 RL Genomics 0:0-0(0).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD.
 RX MEDLINE=95178848; PubMed=7873884;
 RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
 RT "Allelic variation of the type 2 tumor necrosis factor receptor
 RT gene.";
 RL Mamm. Genome 5:726-727 (1994).
 DR EMBL: X76401; CAAS3981.1; -.
 DR PIR: I48854; I48854.
 DR HSSP: P19438; INCF.
 DR MGD: MGI:1314883; Tnftrsf1b.
 DR GO: GO:0007166; P:cell surface receptor linked signal transdu. .; IMP.
 DR GO: GO:0006954; P:inflammatory response; IMP.
 DR GO: GO:0008220; P:necrosis; IMP.
 DR InterPro: IPR001368; TNFR_C6.
 DR Pfam: PF00020; TNFR_C6; 4.
 DR SMART: SM00208; TNFR_C6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS00650; TNFR_NGFR_2; 3.
 DR Receptor.
 KM NON_TER 1
 FT VARIANT 87 87 S -> T.
 FT VARIANT 93 93 T -> I.
 FT VARIANT 268 268 F -> I.
 FT VARIANT 345 345 S -> F.
 FT VARIANT 421 421 Y -> C.
 SQ SEQUENCE 459 AA; 48696 MM; 6C51D2CF1C4626DF CRC64;

Query Match 25.6%; Score 290; DB 11; Length 459;
 Best Local Similarity 33.5%; Pred. No. 3.6e-23;
 Matches 65; Conservative 24; Mismatches 85; Indels 20; Gaps 8;

QY 8 PYASB-NOTCRDQKEYEYEPQHRICSCRCPPGTVYSAKCSRIPTVCATCAENSYNEHMYN 66

Db 16 PYKEPEGYEQCISO EYDRAKQMCACACPCGGQYVKKHCNNTSDIVGCADCSAMWTQVWN 74
 QY 67 YLTIICQLC-RPC--DPVWGLGEIAPCTSKRTQCRCPGFCA--AMALECTHCELLSDC 121
 Db 75 QPRTICLSSSSCSDDV---ETRACTKQNRVCAQMAQSYCAKLHSGNCRQCKLSKCG 130
 QY 122 PGTEALIKDEVKGNHCVCPKAGHFQNTSSPSARCOPTHRCENQGLVEAPGTAQSDTT 181
 Db 131 PGF-GVAASRTSNGNVISACAPGTFSDTTSITVCRPHRIS---TLALPGASTDA 185
 QY 182 CKNPLEPLPPPMSCGT 195
 Db 186 VC---APESPTLS 195

RESULT 6
 Q7YRL5 PRELIMINARY; PRT; 274 AA.
 ID Q7YRL5
 AC Q7YRL5
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CD40.
 GN CD40.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yang S., Sim G.-K.;
 RT "Canine CD40 and CD40 ligand cDNA Sequences";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY333789; AAP8653.1; -.
 SQ SEQUENCE 274 AA; 30284 MM; 9723789A07FAB6DB CRC64;

Query Match 25.1%; Score 284.5; DB 6; Length 274;
 Best Local Similarity 34.9%; Pred. No. 8.4e-23;
 Matches 61; Conservative 18; Mismatches 89; Indels 7; Gaps 4;

QY 9 PYASB-NOTCRDQKEYEYEPQHRICSCRCPPGTVYSAKCSRIPTVCATCAENSYNEHMYL 68
 Db 19 YPEPTACR--EKQYLVDSQ--CNMCCPGEKLVNDCLHTIDTCRCQTGEHDTWNAE 74
 QY 69 TICQLC-RPC--DPVWGLGEIAPCTSKRTQCRCPGFCA--AMALECTHCELLSDCPGTEAE 128
 Db 75 RHCHQHKICDPEVNLGJHVEKXGTSITDTTCDEGLHCTNAA--CESCTWHSICPGLGVK 132
 QY 129 LKDEVKGNHCVCPKAGHFQNTSSPSARCOPTHRCENQGLVEAPGTAQSDTT 183
 Db 133 QIATGISDITICDPELIGFISVSSALSKKHWTSCETGLVKVQAGNKITDVIC 186

RESULT 7
 Q86YK5 PRELIMINARY; PRT; 223 AA.
 ID Q86YK5
 AC Q86YK5
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 5 (Fragment).
 GN TNFRSF5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA He X., Xu L., Zeng Y.;
 RT "Transcripts of CD40 isoform in peripheral mononuclear cells.";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY225405; AA043990.1; -.

DR	GO:	0016020;	C:membrane; IEA.
DR	GO:	00005743;	C:mitochondrial inner membrane; IEA.
DR	GO:	00005488;	F:binding; IEA.
DR	GO:	0004888;	F:transmembrane receptor activity; IEA.
DR	GO:	0006915;	P:apoptosis; IEA.
DR	GO:	0006955;	P:immune response; IEA.
DR	GO:	0007165;	P:signal transduction; IEA.
DR	GO:	0006810;	P:transport; IEA.
DR	InterPro:	IPR006209;	EGF_like.
DR	InterPro:	IPR008063;	Fas receptor.
DR	InterPro:	IPR001993;	Mitoch carrier.
DR	InterPro:	IPR001368;	TNFR c6.
DR	Pfam:	PF00020;	TNFR_c6; 4.
DR	PRINTS:	PRO1680;	FASRECEPTOR.
DR	SMART:	SMO0208;	TNFR; 4.
DR	PROSITE:	PS01186;	EGF_2; 1.
DR	PROSITE:	PS00215;	MITOCH CARRIER; 1.
DR	PROSITE:	PS00652;	TNFR_NGFR_1; 1.
DR	PROSITE:	PS50050;	TNFR_NGFR_2; 4.
DR	Receptor:		
KM	FT	NON TER	
DR	SEQUENCE	223 AA; 223	85C63C20BC4E0B1C CRC64;
DR	SEQUENCE	223 AA; 223	85C63C20BC4E0B1C CRC64;
DR	Query Match	24.5%;	Score 278; DB 4; Length 223;
DR	Best Local Similarity	35.0%;	Pred. No. 3.5e-22;
DR	Matches	62; Conservative	20; Mismatches 83; Indels 12; Gaps 5
QY	7	PPYASENQTCDQDEKEVEYEPQHRICCSRCPEGTYSAAKSRIRDTVCATCAENSTNEHWN	66
DB	22	PTPTA-----CR--EKQYVLSNQ--CCSLQPGQKLVSDCTEFTEIECLPCGSESEFLDTWN	72
QY	67	YLTIQCLPCPCDPVWGLEIAPCTSKRTQCRQCPMPFANALBETHELLSDCPGTE	126
DB	73	RETHCHQHKXCDDPNLGLRVQOKGTSTDTICTCEBGMHGTSEA--CESCVLHRSQSPGFG	130
QY	127	AEIKDEVGKANNHCVCCKXGHPQNTSPSARCQPHTRCENOGVLEAPGTAOSDTTC	183
DB	131	VK-QIATGVSDTICEPCPVGFSSVNSAFERKHPWTSCTKLVLVQAGINKTDVVC	186
DR	131	VK-QIATGVSDTICEPCPVGFSSVNSAFERKHPWTSCTKLVLVQAGINKTDVVC	186
DR	RESULT	8	
DR	ID	088734	PRELIMINARY; PRT; 482 AA.
DR	AC	088734;	
DR	DT	01-NOV-1998	(TEMBLrel. 08, Created)
DR	DT	01-NOV-1998	(TEMBLrel. 08, Last sequence update)
DR	DT	01-JUN-2003	(TEMBLrel. 24, Last annotation update)
DR	DE	P80	TNF-alpha receptor.
DR	GN	TNFR2.	
DR	OS	Mus musculus (Mouse).	
DR	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
DR	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
DR	OX	NCBI_Taxid=10090;	
DR	RN	[1]	
DR	RP	SEQUENCE FROM N.A.	
DR	RX	MEDLINE=98414512; PubMed=9740674;	
DR	RA	Hurtle B., Segade F., Rodriguez R., Ramos S.S., Iazo P.S.;	
DR	RT	"The Mouse Tumor Necrosis Factor Receptor 2 Gene: Genomic Structure	
DR	RT	and Characterization of the two Transcripts."	
DR	RL	Genomics 52:79-98(1998).	
DR	EMBL:	Y14619; CAA74969.1; -	
DR	EMBL:	Y14620; CAA74969.1; JOINED.	
DR	EMBL:	Y14621; CAA74969.1; JOINED.	
DR	EMBL:	Y14622; CAA74969.1; JOINED.	
DR	EMBL:	Y14623; CAA74969.1; JOINED.	
DR	EMBL:	Y14679; CAA74969.1; JOINED.	
DR	HSSP:	Q92956; JMA.	
DR	GO:	GO:0004872; F:receptor activity; IEA.	
DR	InterPro:	IPR001368; TNFR_c6.	
DR	Pfam:	PF00020; TNFR_c6; 4.	
DR	SMART:	SMO0208; TNFR; 4.	
DR	PROSITE:	PS00652; TNFR_NGFR_1; 2.	
DR	PROSITE:	PS50050; TNFR_NGFR_2; 3	

[illegible]


```

SQ  SEQUENCE 283 AA; 30199 MW; 397951C661FE3AA CRC64;
Query Match 21.4%; Score 242.5; DB 6; Length 283;
Best Local Similarity 32.2%; Pred. No. 3.3e-18;
Matches 57; Conservative 18; Mismatches 85; Indels 17; Gaps 6;

OY YASNQTCRDEKEKYEPFOHRICSCRCPPGYVSAKCSRIADTVCATCAENSYNHNNYL 68
DB 35 YAPALPICK-EDDY--FVSGSECPKPGGFHVRQAQGEQGYTCFCECSPTTYLAHFG 90
OY TITCLCPCEPVMGLEIEIAPCTSRKTKQCRCQCPMPCAAW-ALFCHCELLSDCPPTGA 127
DB 91 SKCIQCQCMCDPAMGLIRSRNSTYANALCGSPGHFCTIIQGDHCAACRAVATSPG--- 147
OY 128 ELKDEVGKGNH-----CVPCKAGHFQNTSSPSARCQPHTCENQGLVEAAPTQA 179
DB 148 --GRVQGGTESODTLCONCPGPF--SSNGTLBECQHGKCSKWLVTBAGPGTSS 200

RESULT 14
O72735 PRELIMINARY; PRT; 186 AA.
ID 072735
AC 072735;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE A56R protein.
GN A56R.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OC NCBI_TaxID=10243;
OX (1)
RN RP SEQUENCE FROM N.A.
RC STRAIN=GRI-90;
RX MEDLINE=98229462; PubMed=9568042;
RX Saitonov P.F., Petrov N.A., Riazankina O.I., Totmenin A.V.,
RA Shchelkunov S.N., Saitonov P.F., Totmenin A.V., Petrov N.A.,
RA Ryzankina O.I., Gutarov V.V., Kotwal G.J.;
RT "Species-specific differences in genome organization of cowpox,
RL smallpox, and vaccinia viruses.";
RL Virology 243:432-460(1998).
RN (2)
RN RP SEQUENCE FROM N.A.
RC STRAIN=GRI-90;
RX MEDLINE=97068532; PubMed=8963248;
RX Saitonov P.F., Petrov N.A., Riazankina O.I., Totmenin A.V.,
RA Shchelkunov S.N., Sandakhchiev L.S.;
RT "Genes of a circle of hosts for the cowpox virus.";
RL dokl. Akad. Nauk 349:829-833(1996).
RN (3)
RN RP SEQUENCE FROM N.A.
RC STRAIN=GRI-90;
RA Shchelkunov S.N., Saitonov P.F., Totmenin A.V., Mibeev M.V.,
RA Ryzankina O.I., Petrov N.A., Gutarov V.V., Kotwal G.J.;
RA Sandakhchiev L.S.;
RT "Structure-function and organization of cowpox virus strain GRI-90
RT complete genome.";
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN (4)
RN RP SEQUENCE FROM N.A.
RC STRAIN=GRI-90;
RA Totmenin A.V.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; X94355; CAD90723.1; -.
DR HSSP; Q92956; IMA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6; 2.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
SQ SEQUENCE 186 AA; 20482 MW; D2342F1040A00A83 CRC64;

```

Query Match 21.2%; Score 240; DB 12; Length 186;
 Best Local Similarity 32.2%; Pred. No. 4e-18;
 Matches 48; Conservative 25; Mismatches 66; Indels 10; Gaps 5;

QY 3 PAVAPVYASENOTCDQEKYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENSYN 62
 DB 24 PFLPPLHAPVNSC--DEGEYLDKRHNQCNCPPGEFAKVCSGSDNTKCRCPHYYT 81
 QY 63 EHMNYLTICOLCRPDPVWGLEIAPCTSKRTQCRQPGMFCA--AMALECTHCELLS 119
 DB 82 AIPVNSGCHQCRKC-PTGSPDKV-KCTGTQNSKCSCLPGWYCATDSQTEPCRDVCPKS 139
 QY 120 DCPGTEALKDEVEGKNNHCVPCKAGHF 148
 DB 140 RCPGTFGIDEG--GNPICKSCCVGEX 165

RESULT 15

Q7T2H3 PRELIMINARY; PRT; 318 AA.
 AC Q7T2H3;
 DT 01-OCT-2003 (TREMblrel. 25, Created)
 DT 01-OCT-2003 (TREMblrel. 25, last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, last annotation update)
 DE Tumour necrosis factor receptor.
 GN TNFR.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_taxid=8022;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head kidney;
 RA Zou J., Secombes C.J.;
 RT "Molecular cloning and expression analysis of a TNF receptor homologue
 in rainbow trout, *Oncorhynchus mykiss*,"
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ517804; CAD57165.1; -
 KW Receptor.
 SQ SEQUENCE 318 AA; 35254 MW; 78F8135011283B43 CRC64;

Query Match 21.1%; Score 238.5; DB 13; Length 318;
 Best Local Similarity 29.1%; Pred. No. 1e-17;
 Matches 50; Conservative 22; Mismatches 89; Indels 11; Gaps 3;

QY 16 CRDQEKYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENSYNHMNYLTICOLCR 75
 DB 6 CKTEEYLHDASGVKRCRCRKGQYRTDQGSTKTECFQHEHYTAEINFLKQCLPCR 65
 QY 76 PCDPVWGLEIAPCTSKRTQCRQPGMFCAAMALECTHCELLSDCPPGTEALKDEVGK 135
 DB 66 VCYSNSNQVLRCECASSDRQCVCKTGYCTDGG--CEHCLPVTLCPLSGV----VWQ 118
 QY 136 GNNH---CVPKAGHFONTSSPSARCCPHTRCENQGLVEAAPGTASDPTTC 183
 DB 119 AMPQNDTVCAFCQPGTYNSFNDAFTHCQSHTRCGDLGKEVKSAGTETTDVAVC 170

Search completed: August 27, 2004, 21:10:26
 Job time : 120 secs

